

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 133..189
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2
seq FGCTFVAFXPFA/LS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

```

AGTCTGGGGG TGACATTGCA CCGCGCCCCT CGTGGGGTCG CGTTGCCACC CCACGCGGAC   60
TCCCCAGCTG GCGCGCCCCT CCCATTGCC TGTCCTGGTC AGGCCCCCAC CCCCCTTCCC   120
ACCTGACCAG CC ATG GGG GCT GCG GTG TTT TTC GGC TGC ACT TTC GTC GCG   171
          Met Gly Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala
                   -15                               -10

TTC DGC CCG GCC TTC GCG CTT TCH TTG ATC ACT GTG GCT GGG GAC CGT   219
Phe Xaa Pro Ala Phe Ala Leu Ser Leu Ile Thr Val Ala Gly Asp Arg
   -5                   1                   5                   10

GGG
Gly                                     222

```

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 80..181
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.2
seq LWSSCWLA PLADG/ML

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

```

AAGATGAAGA GGAGGCDGTG GCAGTGGTGG AAGAAGAGGC GCGGCGGCGG GGGTAGGGAG      60
CCTGGAAACG CGAGCGGGG ATG GTA GGT GGT TTG GAC CCG CCG GGC CGC CGT      112
           Met Val Gly Gly Leu Asp Pro Pro Gly Arg Arg
                               -30                    -25
CGT TTC CAG AAA GGG TTT GAC TGG AGG AAC CTC TGG AGC AGC TGT TGG      160
Arg Phe Gln Lys Gly Phe Asp Trp Arg Asn Leu Trp Ser Ser Cys Trp
           -20                    -15                    -10
CTG GCT CCT CTG GCT GAT GGC ATG TTG AGG TAC ATG GGC CAG CVG CAG      208
Leu Ala Pro Leu Ala Asp Gly Met Leu Arg Tyr Met Gly Gln Xaa Gln
           -5                      1                      5
CGA NGG GCA TCC AAT CCA GAG GGG TCC ACT CTA GAG GCC AGG CCA CCA      256
Arg Xaa Ala Ser Asn Pro Glu Gly Ser Thr Leu Glu Ala Arg Pro Pro
    10                      15                      20                      25
GCA CCA TRG GCC AGT GTG TCA CCA AGT GTA AKH MTC CCT CAT CGA CCC      304
Ala Pro Xaa Ala Ser Val Ser Pro Ser Val Xaa Xaa Pro His Arg Pro
           30                      35                      40
TGG GCA GCA AAA ATG GAG ACC GTG AGC CCA GCA ACA AGT CRC ATA GCA      352
Trp Ala Ala Lys Met Glu Thr Val Ser Pro Ala Thr Ser Xaa Ile Ala
           45                      50                      55
GGC GGG
Gly Gly
                                           358

```

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 110..172
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1
seq SLLVVSCFYQISG/RW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

ATAGAACTAC	TGCGGAACCT	CAAAATCAGT	AGATTTGGAA	GTGATTCAAA	GCTAAACTTT	60
TTCCTTGGCC	CTCCKTGTGT	TCTAATTGCT	TTGCAAGTGT	AAKACTAGG	ATG TCC AAG	118
					Met Ser Lys	
					-20	
ATG CCA GTT TTT GCT TCT TTG TTA GTT GTC AGC TGC TTT TAT CAA ATT						166
Met Pro Val Phe Ala Ser Leu Leu Val Val Ser Cys Phe Tyr Gln Ile						
	-15		-10		-5	
TCA GGC CGC TGG						178
Ser Gly Arg Trp						
	1					

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 136..180
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.1
seq VTOLLFPSSPDSA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

AACAAAGAGA	CACAGACAGG	GGACTGTCAG	CYGGYACCGG	AGGMGCGGAC	AACGAGTTAT	60		
CAGCAACTSA	AAGCACCTGA	BGGGCCGCAC	ATTCCANCCC	CAGCCCAGTC	CTCGTCCTCC	120		
ACGCCAGCNC	CAAGC	ATG TSA	GTA ACC	CAA CTT	CTC CCT	TTC TCC	TCC CCA	171
		Met Xaa	Val Thr	Gln Leu	Leu Pro	Phe Ser	Ser Pro	
		-15		-10			-5	
GAC TCT	GCG GGT	CCT TTT	CTG TCC	CCT TTC	TCT			204
Asp Ser	Ala Gly	Pro Phe	Leu Ser	Pro Phe	Ser			
	1		5					

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
(B) TYPE: NUCLEIC ACID

- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..102
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1
seq SFHFLPWALGAMA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

ATG GGG AAA GCA TGG CAA GAG ATG AGG GTG GAA TGG GGG GCA GAC AAG	48
Met Gly Lys Ala Trp Gln Glu Met Arg Val Glu Trp Gly Ala Asp Lys	
-30 -25 -20	
GGG AAT GTC AGA AGC AGC TTC CAC TTT CTC CCC TGG GCA CTG GGA GCC	96
Gly Asn Val Arg Ser Ser Phe His Phe Leu Pro Trp Ala Leu Gly Ala	
-15 -10 -5	
ATG GCA AGT TCA GAG CAG GGG AAG GAG AGG TCC AAC TTG TGC TTT AGG	144
Met Ala Ser Ser Glu Gln Gly Lys Glu Arg Ser Asn Leu Cys Phe Arg	
1 5 10	
AAG ACT CCT CTG GCT ATC ACG GGG AGA GGA ATT GCC AGG AGA CCA GGG	192
Lys Thr Pro Leu Ala Ile Thr Gly Arg Gly Ile Ala Arg Arg Pro Gly	
15 20 25 30	
GGA GGT TGG ATG GGA ATG TGG GTG	216
Gly Gly Trp Met Gly Met Trp Val	
35	

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 2..142
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1
seq VIRLSQFLLKCWP/RT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

A ATG AAA GTG ATG ATG AGG AAG AGG AAG AAA AAG GAC CAG TGT CTC CCA 49
 Met Lys Val Met Met Arg Lys Arg Lys Lys Lys Asp Gln Cys Leu Pro
 -45 -40 -35

GGA ATC TGC AGG AGT CTG AAG AGG AGG AAG TCC CCC AGG AGT CCT GGG 97
 Gly Ile Cys Arg Ser Leu Lys Arg Arg Lys Ser Pro Arg Ser Pro Gly
 -30 -25 -20

ATG AAG GTT ATT CGA CTC TCT CAA TTC CTC CTG AAA TGT TGG CCT CGT 145
 Met Lys Val Ile Arg Leu Ser Gln Phe Leu Leu Lys Cys Trp Pro Arg
 -15 -10 -5 1

ACA AGT CTT ACA GCA GCT ACG 166
 Thr Ser Leu Thr Ala Ala Thr
 5

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 254..361
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq SFSIXTLLWGLNC/KR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

ACTGTTTTAG TGTTTTGAAT ATCTTCTTCC AGAGTTTGAT GTATATGTAT CTTGGAGGTA 60

TATGTATTTT TAATTATATA AATATTTGAC CCTCTTTGCC TARTTTGTTT TATTCAC TTC 120

AACTTTGACC CTTTATACTT CTTTTTAAAT TTCAC TTTCT TATGGTTGTT TTTCTACTTT 180

TCCTCAATGC CCTTTGTAAA ATTTTCATTT GAATCTATTA TTCTCCCTTG GACGTCTTAA 240

TTCCTTCTCT ACT ATG ACT TTT TCT TTC TTT TGT TTC TTT CCT GGG TTC 289
 Met Thr Phe Ser Phe Phe Cys Phe Phe Pro Gly Phe
 -35 -30 -25

AAG CCA CTC CTG TTT CAT TAC TTT CTT TTT WNK TCC TTT TCT ATT TKD 337
 Lys Pro Leu Leu Phe His Tyr Phe Leu Phe Xaa Ser Phe Ser Ile Xaa

[illegible]

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 11..133
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5
seq RLLLLILSGCLVYG/TA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

[illegible]

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 58..153
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq PLLSCSCPPPLLG/EG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

```

ACTTCCACGG GACCCACCAG CTAAATGCC GGCAGCCCTG GGACTTCTGG CCTCACA      57
ATG GTT GAG ATG ACT GGG GTG TGG CAG TGC CAA GCC GAG GCT GTG AAA      105
Met Val Glu Met Thr Gly Val Trp Gln Cys Gln Ala Glu Ala Val Lys
      -30                      -25                      -20

GGC CTT CCA CCT TTA CTC TCG TGC TCG TGC CCT CCC CCA TTG TTA GGA      153
Gly Leu Pro Pro Leu Leu Ser Cys Ser Cys Pro Pro Pro Leu Leu Gly
      -15                      -10                      -5

GAA GGG CAT GCT CAG GCC AGC CCA TTA GCC CAG GAG GAG GAC AAG AAA      201
Glu Gly His Ala Gln Ala Ser Pro Leu Ala Gln Glu Glu Asp Lys Lys
      1                      5                      10                      15

CAC ACG GAG CAG ACA CAA GCC ACC TCA CCA ACC CAG CCT      240
His Thr Glu Gln Thr Gln Ala Thr Ser Pro Thr Gln Pro
      20                      25

```

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 59..121
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5

seq AGLLP LLLGNAPG/ES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

```

AATTTGCTCA CACCCAGCAG GCAGAGAAGG CAGCAGCAGG CAGGACCGCC ACCCTCCC      58
ATG CAA ATC ACC CCC GGG AGT GCA GCT GGG CTC CTC CCG CTC CTC CTA      106
Met Gln Ile Thr Pro Gly Ser Ala Ala Gly Leu Leu Pro Leu Leu Leu
  -20                -15                -10

GGC AAT GCT CCT GGG GAG TCT GTT GGG GGA AGA TGC SAT CCA GGG TGC      154
Gly Asn Ala Pro Gly Glu Ser Val Gly Gly Arg Cys Xaa Pro Gly Cys
  -5                1                5                10

TGG                                          157
Trp

```

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 152..202
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq TWLLLTLQNSVFT/SF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

```

AGAATTTTGC TGGGAATTAA TATTAAATAC TCACTGGAAT TTATCTTTAC CAACTTTAGT      60
GGAATTCAGC CTATCTACAG CTCTCCTTTC CACTTTGTTT CTCAGAAATT CTCAGCAATG      120
GTTTCATGAA CCACTGGGAG GTCATTTGCC T ATG ATT TTG TCC ACC TGG CTC      172
                               Met Ile Leu Ser Thr Trp Leu
                               -15

TTA CTT ACC CTT CAA AAC TCA GTA TTT ACA TCT TTC AGG ATA TCT CCC      220
Leu Leu Thr Leu Gln Asn Ser Val Phe Thr Ser Phe Arg Ile Ser Pro
-10                -5                1                5

AAC AGA ATA CAA AGT ATG CTA CCT CCC ATG      250
Asn Arg Ile Gln Ser Met Leu Pro Pro Met
  10                15

```

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 33..128
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq VCIVLALCHTSRP/MS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

AAATCTCTTC TAATCCTCCT TAATGCATTT TG ATG GCT TTT CAT AGC TAT TGG	53
Met Ala Phe His Ser Tyr Trp	
-30	
GGA AAA AGT TTA CAA TCC TTT AAG ACG TTC ATG AGA GTC TGC ATT GTC	101
Gly Lys Ser Leu Gln Ser Phe Lys Thr Phe Met Arg Val Cys Ile Val	
-25 -20 -15 -10	
TTG GCC CTT TGC CAC ACA TCC AGA CCC ATG TCT TAC CAT GTT CCC CTG	149
Leu Ala Leu Cys His Thr Ser Arg Pro Met Ser Tyr His Val Pro Leu	
-5 1 5	
GCT GCT GGC TCC CCA CTC ATG CAC TGG TCT CCT TGT AGT CCT GTG CCC	197
Ala Ala Gly Ser Pro Leu Met His Trp Ser Pro Cys Ser Pro Val Pro	
10 15 20	
TTC ATT GGG	
Phe Ile Gly	206
25	

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 113..160
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq RFTLLPLVLHSQS/SC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

```

ATTCTCGTA AATGATGAGA TGGGGTTAAA TGGTTTTCGA GAAATATGTG AGAGGTAATG    60
TGAAATAAGT TACTTTAAGA AGGCCTGGCC CTGGTAATGT CGTTACCAGC TG ATG AAG    118
                                         Met Lys
                                         -15

TTG CGG TTT ACC TTG CTG CCC CTG GTG CTA CAT TCA CAA AGC AGC TGT    166
Leu Arg Phe Thr Leu Leu Pro Leu Val Leu His Ser Gln Ser Ser Cys
          -10                    -5                      1

GTC TTT TGG AAA GCC GGG    184
Val Phe Trp Lys Ala Gly
          5

```

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 4..93
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq FIPFLVIYSFVLS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

```

ACC ATG ATG ATC ATT CTG GGG TTT GCT TTT TGC CCT GGT CAC TTT AGG    48
Met Met Ile Ile Leu Gly Phe Ala Phe Cys Pro Gly His Phe Arg
-30                    -25                    -20

TTT AAT TTT ATT CCA TTC CTG GTC ATT TAC AGT TTT GTT CTG TCA TCT    96
Phe Asn Phe Ile Pro Phe Leu Val Ile Tyr Ser Phe Val Leu Ser Ser
-15                    -10                    -5                      1

CCC CAT ACC CAT CGA GAA CCC TAT TCT CCT GTG GCA GAC TTT AAT GAA    144
Pro His Thr His Arg Glu Pro Tyr Ser Pro Val Ala Asp Phe Asn Glu
          5                      10                      15

```

TGT AAC CGC AGT
Cys Asn Arg Ser
20

156

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 198..278
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq CLLSYIALGAIHA/KI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

```

AACTTTGCCT GGGTGTCTTG CGTTCCTGCAC ATTCCGGAGG ACCAGCTTCC CCATCAGAAG   60
TCTGACTCCA TGGAAACCAG ATGGGGCAAC GGGGTGGTTC TAGTGCAGAC TGTAGCTGCA   120
GCTCCTCTCC ACCTCTAGCC TGCTCATTTT CAGCTCAGAA ATTCTACTAA TGGCGTTTTT   180
TCTTCCTGAA AAAGGAA ATG AAC AGG GTC CCT GCT GAT TCT CCA AAT ATG       230
      Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met
      -25                               -20
TGT CTA ATC TGT TTA CTG AGT TAC ATA GCA CTT GGA GCC ATC CAT GCA       278
Cys Leu Ile Cys Leu Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala
  -15                               -10                               -5
AAA ATC TGT AGA AGA GCA TTC CAG GAA GAG GGA AGA GCA RRT GCA AAG       326
Lys Ile Cys Arg Arg Ala Phe Gln Glu Glu Gly Arg Ala Xaa Ala Lys
  1                               5                               10                               15
ACG GGC GTG
Thr Gly Val

```

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 195..239
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq LFLNLPLVIGTIP/LH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

```

AATATGTAAA TGTACTATAC AGAATTATAC ATAAAAGAGA AACTTTTCAT GTATGTAAGT    60
TTAAAAATGA AGTAAATGGG GGTTCCAAAT AACATTARAA TTGGTTATGA GTTTTGTAAA    120
AGGAAATCAT ACTTGGCATT CTAACTTAA TATTTCTTTG CAATGTTTAG GTATATGTGG    180
ATATTCCTGG AGCT ATG GAT TTA TTT CTT AAT TTG CCA CTT GTC ATC GGT    230
          Met Asp Leu Phe Leu Asn Leu Pro Leu Val Ile Gly
          -15                      -10                      -5

ACC ATT CCT CTA CAT CCA TTT GGT AGC AGA ACC TCA AGT GTA AGC AGT    278
Thr Ile Pro Leu His Pro Phe Gly Ser Arg Thr Ser Ser Val Ser Ser
          1                      5                      10

CAG TGT AGC ATG AAT ATG AAC TGG CTC AGT TTA TCA CTT CCT GAA    323
Gln Cys Ser Met Asn Met Asn Trp Leu Ser Leu Ser Leu Pro Glu
    15                      20                      25

```

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 11..229
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq VIRSTLVLSQCLC/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

AAAATATTAA ATG GMA AAA AAT CAC AGA AAT AAA AAA TCC ATA CAT TTT Met Xaa Lys Asn His Arg Asn Lys Lys Ser Ile His Phe -70 -65	49
CCA CTG TGC ACC ATT CCA AGT AGM ATG MTG AAA TCT TGT ACT CTC CCA Pro Leu Cys Thr Ile Pro Ser Xaa Met Xaa Lys Ser Cys Thr Leu Pro -60 -55 -50 -45	97
CTT CAG CGC ACC TGG GAC ATS MAT CCT TCC TTT GTC CAT TGG AWC CAA Leu Gln Arg Thr Trp Asp Xaa Xaa Pro Ser Phe Val His Trp Xaa Gln -40 -35 -30	145
GCC CGY CTA CAA TCC CCA CCG YCT AGT CAC TTA GTA SCC CTC TCG GTG Ala Arg Leu Gln Ser Pro Pro Xaa Ser His Leu Val Xaa Leu Ser Val -25 -20 -15	193
ATC AGA TCG ACT CTC GTG CTA TCC CAG TGC TTG TGT TCA AGG MAC CCT Ile Arg Ser Thr Leu Val Leu Ser Gln Cys Leu Cys Ser Arg Xaa Pro -10 -5 1	241
TAT TTT AGT GCA ATG ATG ACC CCA AAG TGC AAG AGT ATT GMT GCT GGC Tyr Phe Ser Ala Met Met Thr Pro Lys Cys Lys Ser Ile Xaa Ala Gly 5 10 15 20	289
AAT TCA GGT ATG CCA AAG AGA AAC TGT AAA GTG CTT CCT TCA AGT GAA Asn Ser Gly Met Pro Lys Arg Asn Cys Lys Val Leu Pro Ser Ser Glu 25 30 35	337
AAG ATG MAA GTT CAC Lys Met Xaa Val His 40	352

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 317..358
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq SFIALVYSSLSFQ/KV

(xii) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

```

AGAGCAAAGC AGACAGAAAT TCCTCTGGTT CTGTAGAGCT GACAATTCAT TAATGTGAGG    60
TAGTCAATAA CAAATATATT TTATGTCAAG TGGTGRATGG DTYCDATTGA AGAAAAATGA    120
CTCAATAAGA GGAGAGAAAA TGATGGTATG TGTATGGTGG GTAGGTGTGC GTGATGCTGT    180
TTTGGATAGC GAGGCCTCCG ATTAGATGCT ACGTGAGCAG GGACCCAAAA GAGCCATGTG    240
TTTCATCTAC CTGGGGGAGA AGCCTGCTGG CAGATCCTGT TGAACACTCG TTACCTAAAT    300
CTCTTGCATT GGCTCC ATG TCA TTT ATT GCT CTA GTG TAT TCT TCA CTA TCT    352
          Met Ser Phe Ile Ala Leu Val Tyr Ser Ser Leu Ser
                    -10                               -5

```

```

TTT CAG AAA GTG CCA GGG                                370
Phe Gln Lys Val Pro Gly
      1

```

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 93..158
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq IVLFLNSXFPIIC/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

```

ATAATATAGA TCTTTAATTT CTCTCAGCAA TGATTATAGT TCACAATGTG GAGGATTTAC    60
ATGTCTTTCA TTAAATTTAT CCAAAGTACT TT ATG GTT TTT GAT ACT TTA AAA    113
          Met Val Phe Asp Thr Leu Lys
                    -20

AGT AGA ATT GTT CTT TTT TTA AAT TCG RWT TTC CCA ATC ATT TGC AGC    161
Ser Arg Ile Val Leu Phe Leu Asn Ser Xaa Phe Pro Ile Ile Cys Ser
-15              -10              -5              1

CGG                                164
Arg

```

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 68..244
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq IFLFSILLMSLRT/FH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

```

AAAGCACAGA TGGCAGTCCA TTCATTGAAG ATGGTTTTTT TCAAGGTGAG TGTGGTCTT      60
TTGCACA ATG CTT GAG ATG GAA ATG ACT TGG CTG AGA CTA TGT GAT GAG      109
      Met Leu Glu Met Glu Met Thr Trp Leu Arg Leu Cys Asp Glu
                        -55                                -50
TGC TCC AGA TGG GGC ATG GCA TCG GCA TGG GGT AGG GGT GGA AAG CTT      157
Cys Ser Arg Trp Gly Met Ala Ser Ala Trp Gly Arg Gly Gly Lys Leu
-45                        -40                                -35                                -30
CTT GGA GCT CAA GTA GCC CTT CAT CCT AGA AAC TGC AGC AAA GCT AAG      205
Leu Gly Ala Gln Val Ala Leu His Pro Arg Asn Cys Ser Lys Ala Lys
                        -25                                -20                                -15
ATC TTC CTG TTC AGT ATT TTA TTA ATG TCT TTA AGA ACT TTT CAC TGT      253
Ile Phe Leu Phe Ser Ile Leu Leu Met Ser Leu Arg Thr Phe His Cys
                        -10                                -5                                1
AAT TAT TTC AGA GGC AAT GGG
Asn Tyr Phe Arg Gly Asn Gly
      5                                10

```

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 104..154
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.7
 seq MLFFLGALCRESG/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

```

AACAAAGGAG GGAAGGGTTA GAGTGAGGTA CTCACCCAGA GAAGAGCTGT CCCGGCCTGG      60
GGGTCCCATT CGTCCCTTCT CTTTCTTGCC AAAGAGACGG CCT ATG GAT GAC TTG      115
                               Met Asp Asp Leu
                               -15

ATG CTC TTC TTC TTG GGG GCT TTG TGC AGA GAA TCT GGG GTG CCC TCA      163
Met Leu Phe Phe Leu Gly Ala Leu Cys Arg Glu Ser Gly Val Pro Ser
          -10                      -5                      1

CTG GGA AAG CAG GAG AGA ATG AGA GCA TAT GCT GCT GAG ATG CCC CCT      211
Leu Gly Lys Gln Glu Arg Met Arg Ala Tyr Ala Ala Glu Met Pro Pro
          5                      10                      15

CTC CTC CCA AGT CCT TGT CCA CCC CCT TCT CAT CTT CCC AAG CCA GCT      259
Leu Leu Pro Ser Pro Cys Pro Pro Pro Ser His Leu Pro Lys Pro Ala
          20                      25                      30                      35

TCT CCC TGT CCC TAT CCC TTG NNC CTG CTG ACC TTC CCC GTG GGG GTC      307
Ser Pro Cys Pro Tyr Pro Leu Xaa Leu Leu Thr Phe Pro Val Gly Val
          40                      45                      50

CCC CAT CTT CCA GGG ACC CGC CTG CAG TGC CAA GGC CTG GGT CAT TCT      355
Pro His Leu Pro Gly Thr Arg Leu Gln Cys Gln Gly Leu Gly His Ser
          55                      60                      65

CTC ARA CGG GCA GAG CGG GGA GTG GGT GGT GGG GTG TCT CCT GGG      400
Leu Xaa Arg Ala Glu Arg Gly Val Gly Gly Gly Val Ser Pro Gly
          70                      75                      80
  
```

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 13..87
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: . score 4.6
 seq LPTLLLLPVGAPG/KK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

ATCGAATGCA GA ATG GTT TTG GGA GCC CTG AAC CTT CCC TCC CAG GAA CTC	51
Met Val Leu Gly Ala Leu Asn Leu Pro Ser Gln Glu Leu	
-25 -20 -15	
CCC ACT CTC CTG CTC CTC CCA GTG GGG GCA CCT GGR AAG AAA AAA GGC	99
Pro Thr Leu Leu Leu Leu Pro Val Gly Ala Pro Gly Lys Lys Lys Gly	
-10 -5 1	
ATG GAA GGC AAA ACT CCC TTG GAC CTG TTT GCT CAT TTT GGC CCT GAG	147
Met Glu Gly Lys Thr Pro Leu Asp Leu Phe Ala His Phe Gly Pro Glu	
5 10 15 20	
CCA GGG GAC CAC TCA GAT CCG CTG CCT CCC TCT GCA CCC TCT CCC ACT	195
Pro Gly Asp His Ser Asp Pro Leu Pro Pro Ser Ala Pro Ser Pro Thr	
25 30 35	
CGG GAG GGG GCT CTG ACC CCG CCC CCA GGG	225
Arg Glu Gly Ala Leu Thr Pro Pro Pro Gly	
40 45	

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 207..263
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.6
 seq QTFVSFLSIPVLG/LV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

ATACACCTCC ATTTTAAATG TGCTGCAATA TGAATGAAGT GACCTGTGTT TCATCACTTG	60
TTCAAATGAT TCTTATCCAT GTTTTGTAC TTAGTAAGGG CCATACGTAG TGGGATTAAA	120
TATTTGTGCC CTTGCTTTGA AAACAAACT GAAAGTGAAT GACACATAAG GGCAGGGATT	180

TCAGAACAGA TTTTCTTGA ATAAAA ATG CTT GTG TCA AAA ATT CAA ACA TTT 233
 Met Leu Val Ser Lys Ile Gln Thr Phe
 -15

GTC TCT TTC CTT TCC ATT CCA GTT CTA GGT CTC GTT CCA GAT CAT ATT 281
 Val Ser Phe Leu Ser Ile Pro Val Leu Gly Leu Val Pro Asp His Ile
 -10 -5 1 5

CTC CAG CTC ATA ACA GAG AAA GAA ACC 308
 Leu Gln Leu Ile Thr Glu Lys Glu Thr
 10 15

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 188..280
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq LLSTGLNILGTQA/FR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

ATCATAGTCA CTTTCCAAGT TTATGACCCA GAGCAATCTG ACCTTGGTAG CTGTCTCCC 60

TCATTAAATT CTCTGACTTC ATAATCAGCT CACATTCCTT TCCTCTCTTT CCCTCTCTTT 120

TTAAATATCT GTAAACATT CAAATTGATC CACGTAGATT TATCTTGCTT TTAGGCCACA 180

CTCTGAG ATG TGT AAT CCG GTT GCT CAC ACA TTT AGA GGA GTC CAT GAG 229
 Met Cys Asn Pro Val Ala His Thr Phe Arg Gly Val His Glu
 -30 -25 -20

CAT CAC GCC ATG CTA CTC TCC ACT GGT TTG AAC ATC TTA GGC ACT CAG 277
 His His Ala Met Leu Leu Ser Thr Gly Leu Asn Ile Leu Gly Thr Gln
 -15 -10 -5

GCA TTC CGT TAC GAA GAT GGG CAG CTG 304
 Ala Phe Arg Tyr Glu Asp Gly Gln Leu
 1 5

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 126..176
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq ILLWEACTGRCQA/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

```

TATTCAGTTG GGGGCAAGCC AGCCATGATG TGGACCTTTC ATTGGGTAGG GCAAGTCCCC    60
AAAGTTGGAA AAATGGAAAG TGGGAGCTGT GAGGCACGTG TTACACCCAC ACTTTCCTCC    120
TACAG ATG CAG TGT TGG ATT TTG TTG TGG GAG GCA TGC ACA GGT AGG TGC    170
  Met Gln Cys Trp Ile Leu Leu Trp Glu Ala Cys Thr Gly Arg Cys
        -15                -10                -5

CAG GCC TCC CTA CTC TCT CCC TGG CCC AGA GGT GGC AGG GGC AAG TTA    218
Gln Ala Ser Leu Leu Ser Pro Trp Pro Arg Gly Gly Arg Gly Lys Leu
        1                5                10

GTG GCA GTG GTG GCT GCA AAA TGG TTG GCA GCA ATC TGT GGG ATT TGG    266
Val Ala Val Val Ala Ala Lys Trp Leu Ala Ala Ile Cys Gly Ile Trp
    15                20                25                30

GCT ATC AAA GAA ATG CCA AGC CAT GGC CAC AGT CTT CAA GCA GGG GCA    314
Ala Ile Lys Glu Met Pro Ser His Gly His Ser Leu Gln Ala Gly Ala
        35                40                45

GGG GAA GGT GCA CTG GTG ACC TGG AGC CTG CAA ACC TCA TTT GGT GTG    362
Gly Glu Gly Ala Leu Val Thr Trp Ser Leu Gln Thr Ser Phe Gly Val
        50                55                60

AAG CAG TAT AAG TGG GGA GTT GTG TGG CAT GAA GCA AAC CTG TTG CTT    410
Lys Gln Tyr Lys Trp Gly Val Val Trp His Glu Ala Asn Leu Leu Leu
        65                70                75

```

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 149..223
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq VLCILGCHGNLCC/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

```
ATTTTAGAAA GTAAGGAAAT AAAACTTTAA TTGAAGTTGG AATAAACTCA GTTCTGAGCA    60
TTCCATTCTA CTCTGCAGTT GTCATTTATA GACAGCTGTG GATCATAATA CCTATAGACT    120
AGATATCGTT ATCTACTTAT TTATATTA ATG ACA GGA TAT CCC TGG GCA AAC    172
                Met Thr Gly Tyr Pro Trp Ala Asn
                -25                      -20
AGC ATC ACC ACT GTA CTG TGT ATT CTT GGT TGT CAT GGG AAC CTT TGC    220
Ser Ile Thr Thr Val Leu Cys Ile Leu Gly Cys His Gly Asn Leu Cys
    -15                      -10                      -5
TGT GAA CCA GCA GTG AGA GCA CTC GGG    247
Cys Glu Pro Ala Val Arg Ala Leu Gly
    1                      5
```

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 475..546
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq IFTALFLXLHSA/IN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

```
AAATTATGGA TGCCTACCAT CTACCAGGTA CTGTTCTAGC TACAAGGAAT AACTAAAAAT    60
```



```

AGGTAAACAA AACAGATGAA AAACCTAGAA ATTTATACTG ATGTTATCAG AGTAATGTTT 120
AATTTTTCAG ATAATTGTTA TGTCTAAATT AGCATTGAT TTTTCAATTA AGAATTTTTA 180
AATTATCCAA TATTGCAAGC ATATATAGAA ACATGGAAAA CAACAAAATT CTCATGCATA 240
TACTTCAAAC ACAGAGCTAA CAGATGTTAT TATTTTTTAT TTCTTTCACA ACCCAACTTT 300
CGGGAAACAA AATAGGCACA GCAAACTGG GATCTCCTCA TCCCCTTCTC CTTTCTTATA 360
TAAAAGTAAT CCTGCTCTTG GTACAGCTAT GTATCATACT CATCCAGGTT TTAATTTTTC 420
TTATATAACG GAACATATAT GGTGTTATTT TACGGATTTT AAAGCTTTAC ATAA ATG 477
                                         Met
GTG TCA TGT GAT GTW CVN TCT TAT GTG ATC ATT TTT ACT GCA CTC TTT 525
Val Ser Cys Asp Val Xaa Ser Tyr Val Ile Ile Phe Thr Ala Leu Phe
      -20                      -15                      -10

TTA WTG CTG CAT AGT GTG GCA ATA AAT GAA GAG TTT 561
Leu Xaa Leu His Ser Val Ala Ile Asn Glu Glu Phe
      -5                      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 80..139
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq LFAIFLMCLKSIG/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

```

ATGATAAGGG CTTATTCACA TTATTCATTC TTGAATGAAT TTTGATAGTG TCTGTCTTTC 60
AGGAACTTTG TCCTAAGTA ATG AAA TCC TTT GAT AAA AAG TTG TTT GCA ATA 112
          Met Lys Ser Phe Asp Lys Lys Leu Phe Ala Ile
          -20                      -15                      -10

TTT CTT ATG TGT TTA AAG TCT ATA GGT TCT GTG GTG ATG CCC CAG CCG 160
Phe Leu Met Cys Leu Lys Ser Ile Gly Ser Val Val Met Pro Gln Pro
      -5                      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 36..134
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5
seq LASLFGLDQXAXG/HG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

ATTTTCCTCC CCGCAACCTG GTGAAAGCCA AYKCA ATG TTC GGT GCG GGG GAC	53
Met Phe Gly Ala Gly Asp	
-30	
GAG GAC GAC ACC GAT TTC CTC TCG CCG AGC GGC GGT GCC AGA TTG GCC	101
Glu Asp Asp Thr Asp Phe Leu Ser Pro Ser Gly Gly Ala Arg Leu Ala	
-25 -20 -15	
TCA CTT TTT GGA CTG GAT CAG GYA GCY SST GGC CAT GGA AAT GAA TTT	149
Ser Leu Phe Gly Leu Asp Gln Xaa Ala Xaa Gly His Gly Asn Glu Phe	
-10 -5 1 5	
TTC CAG TAC ACA GCC CCA AAA CAG CCT AAG AAA GGC CAG GGA ACG GCA	197
Phe Gln Tyr Thr Ala Pro Lys Gln Pro Lys Lys Gly Gln Gly Thr Ala	
10 15 20	
GCA ACA GGA AAT CAG GCA RCA CCA AAA ACA GCA CCA GCC RSC ATG AGC	245
Ala Thr Gly Asn Gln Ala Xaa Pro Lys Thr Ala Pro Ala Xaa Met Ser	
25 30 35	
ACT CCC ACA ATA CTG GTC GCA ACA GCA GTC CAT GCA TAT CGA TAC ACA	293
Thr Pro Thr Ile Leu Val Ala Thr Ala Val His Ala Tyr Arg Tyr Thr	
40 45 50	
RAT GGT CRA TAT GTA AAG CAG GSR AAT TTG GTG CTG CAG TTC TGG	338
Xaa Gly Xaa Tyr Val Lys Gln Xaa Asn Leu Val Leu Gln Phe Trp	
55 60 65	

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 107..190

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.5
seq RFLSLSAADGXDX/SX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

```

AAAGTCAGCG CTGGAGTCGG CTAGGCGGCT GGAAACGGCG GCTGCCGCCG GTGACTCAGG      60
GAGGCGGGAG GCCGMSGGMG GAGCTCTTCC TGCAGGCGTG GARACC ATG GTG CTC      115
                               Met Val Leu
ACG CTC GGA GAA AGT TGG CCG GTA TTG GTG GGG AGG AGG TTT CTC AGT      163
Thr Leu Gly Glu Ser Trp Pro Val Leu Val Gly Arg Arg Phe Leu Ser
-25                -20                -15                -10
CTG TCC GCA GCC GAC GGC ASC GAT GSC AGC CAM GAC AGC TGG GAC GTG      211
Leu Ser Ala Ala Asp Gly Xaa Asp Xaa Ser Xaa Asp Ser Trp Asp Val
                -5                1                5
GAG CGC GTC GCC GAG TGG CCC TGG CTC TCC GGG ACC ATT CGA GCT GTT      259
Glu Arg Val Ala Glu Trp Pro Trp Leu Ser Gly Thr Ile Arg Ala Val
                10                15                20
TCC CAC ACC GAC GTT ACC AAG AAG GAT CTG AAG      292
Ser His Thr Asp Val Thr Lys Lys Asp Leu Lys
                25                30

```

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 429 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 361..411

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.4
 seq LTSVFQAMIWSQG/VS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

```

ATGAAAACAG TTTTCTTTGT GATTTGTCAA TTGATGTTTA AACAGTGTTT ATCCTTCCAG   60
GTAGTATGAT GATGTATTTG TTGGAGACAA ARTATTTGCC CTAGCCTTTT TACTAATATT  120
TCAGATGAGA TTCTGTGGAG GAGAAGCATC TCCCCAAATG TCCTTGTTTT ATAGTAAATA  180
ATTCTACCAC GAGGATCCTT ATCCATAAAT CTATATTCAT GTTTATTTTG TGCTAGATAC  240
AGATCTTGCA ATATTCATGA AGCTTTAAGA AGAGCACTTT GAATCTTAAA AGAGATTCTC  300
TGAGCAGGGG TTGGCAGTGG TGAGGTCCAG GTAGTTATAA TAGCCATAAG AGCAGGGATT  360
ATG GTT ATT GAG CTC ACC AGT GTG TTT CAA GCC ATG ATC TGG AGT CAA   408
Met Val Ile Glu Leu Thr Ser Val Phe Gln Ala Met Ile Trp Ser Gln
      -15                      -10                      -5

GGT GTT AGT GAT TCC TCT AAG                               429
Gly Val Ser Asp Ser Ser Lys
      1                      5
  
```

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 47..196
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq ILFLFYFPAAYYA/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

```

ATDCGCCCCCT GGAGCAAGCC GGGGCCTGGT CGGCARCTGG GCCGCC ATG GAG TCC   55
                                   Met Glu Ser
                                   -50

ACG CTG GGC GCG GGC ATC GTG ATA GCC GAG GCG CTA CAG AAC CAG CTA  103
Thr Leu Gly Ala Gly Ile Val Ile Ala Glu Ala Leu Gln Asn Gln Leu
      -45                      -40                      -35
  
```

GCC TGG CTG GAG AAC GTG TGG CTC TGG RRT SAC CTT TKC TNG SCG ATC	151
Ala Trp Leu Glu Asn Val Trp Leu Trp Xaa Xaa Leu Xaa Xaa Xaa Ile	
-30 -25 -20	
CCA AGK ATC CTC TTT CTG TTC TAC TTC CCC GCG GCN TAC TAC GCC TCC	199
Pro Xaa Ile Leu Phe Leu Phe Tyr Phe Pro Ala Ala Tyr Tyr Ala Ser	
-15 -10 -5 1	
CGC CGT GTR GGC ATC GCG GTG CTC TGG ATC AGC CTS ATC ACC GAG TGG	247
Arg Arg Val Gly Ile Ala Val Leu Trp Ile Ser Leu Ile Thr Glu Trp	
5 10 15	
CTC	250
Leu	

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 196..270
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq VLVGVFLSTFLYC/EC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

ATNCTGTGTT ACTCATTTCC TGTCTCAGAT ACTTTGGATC CCTTGGTTCT GATCTTTCAG	60
GGGGAGAGGG CATGTTAAGA GGAGTAAGTA GATGGATGAT CTTACACAAT TGAACCTCTC	120
TTACCTCTGG CCTTGATATGC TCTTACATAG GCTGTCCCTT CTCTACATTT TCTTATTTAA	180
GGAAAAACAC AGAAC ATG ATT ATT GTC TCA GAA TTA GGA ACC CCT ACT GGT	231
Met Ile Ile Val Ser Glu Leu Gly Thr Pro Thr Gly	
-25 -20 -15	
GTG CTC GTA GGT GTC TTT TTG TCT ACT TTT CTC TAT TGT GAA TGT GTA	279
Val Leu Val Gly Val Phe Leu Ser Thr Phe Leu Tyr Cys Glu Cys Val	
-10 -5 1	
AAG GGG CCG	288
Lys Gly Pro	
5	

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 80..145
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq GFLLCPLVCGLRR/WT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

```
AGCGTTTATG GCCGCGTTAA GTCTGAGTGC CGCTTTGAGT TGTGAATGA AGTGAAGTTC      60
ATTGTGCAGC GTTCGGTTC ATG AAC TGG AAT GTA AGA GGC ACC AGA GGA TTC      112
               Met Asn Trp Asn Val Arg Gly Thr Arg Gly Phe
               -20                               -15
CTG CTC TGT CCC CTG GTT TGC GGC TTG CGA CGT TGG ACA TCC CCG GAT      160
Leu Leu Cys Pro Leu Val Cys Gly Leu Arg Arg Trp Thr Ser Pro Asp
-10                               -5                               1                               5
TGT TGT TTA ATA GAG AAA ACT CAC CGC GGG      190
Cys Cys Leu Ile Glu Lys Thr His Arg Gly
               10                               15
```

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 49..105
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.4
seq RGLLLGLAVAAAA/VR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

```

AAGATAGAGG CCGCAACCTC GGAAGTGC GG ACGGGTGGGC CTATATAG ATG TTG AGG      57
                                     Met Leu Arg

TGC GGA GGC CGT GGG CTT TTG TTG GGC CTG GCT GTA GCC GCA GCA GCG      105
Cys Gly Gly Arg Gly Leu Leu Gly Leu Ala Val Ala Ala Ala Ala
  -15                -10                -5

GTA AGG
Val Arg
  1
                                     111

```

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 95..136
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq ILLMIVFSIFLLL/CN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

```

ACCCAGAGGC AGAAAGTAAT ATTGCTTACT ATGAGTCTAT ATATCCTGGG GAATTTAAGA      60

TGCCAAAGCA GCTCATTCAC ATACAGCGTA AGTA ATG ATT CTC TTA ATG ATT GTA      115
                                     Met Ile Leu Leu Met Ile Val
                                     -10

TTT TCT ATA TTT CTC TTA TTA TGT AAC TTG ACA GAT TTT TAT CTC TTC      163
Phe Ser Ile Phe Leu Leu Leu Cys Asn Leu Thr Asp Phe Tyr Leu Phe
  -5                1                5

AGG AGC GAT GGG
Arg Ser Asp Gly
  10
                                     175

```

(2) INFORMATION FOR SEQ ID NO: 155:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 214 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 149..190
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.4
 seq SLLFIFRSILISC/FS
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

```
ACAATTTGTT TTATAAGCCT ATATTAATTG GGTTTTGACT GAATTAATTA TATAACCATT    60
TATCTCAAAA TGAAATGTTC CATAAAATTT ATTTAAWAGT ATATACTGYA TAAGTGTTAA   120
ATTATGAAAT TTAGTGGTCT TATAGAGA ATG TCT TTA TTG TTT ATT TTT AGG      172
                               Met Ser Leu Leu Phe Ile Phe Arg
                               -10

TCA ATT TTG ATC TCC TGC TTT TCA GGA GAC TTT TTT TTT TTT              214
Ser Ile Leu Ile Ser Cys Phe Ser Gly Asp Phe Phe Phe Phe
-5                               1                               5
```

(2) INFORMATION FOR SEQ ID NO: 156:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 164 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Dystrophic muscle
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 27..77
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.3
 seq SKVLIQLSQAFWA/SP
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

ACCTGGTATG AATTACAAAA CTGTAA ATG CCT TTG ATT AGT AAA GTT TTG ATA 53
 Met Pro Leu Ile Ser Lys Val Leu Ile
 -15 -10

CAG CTA AGC CAA GCA TTT TGG GCC TCA CCT GAG GGT AGG AAC AGT TCT 101
 Gln Leu Ser Gln Ala Phe Trp Ala Ser Pro Glu Gly Arg Asn Ser Ser
 -5 1 5

GGG AGT AAG AGG AAG CAG TTG GTA GCT GCA GTG GAG ATG CGA TAC TGT 149
 Gly Ser Lys Arg Lys Gln Leu Val Ala Ala Val Glu Met Arg Tyr Cys
 10 15 20

AAA AGG CAG CAG GGG 164
 Lys Arg Gln Gln Gly
 25

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 142..228
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq VLLGSTAMATSLT/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

AAGTTGTAAT CCCACTAAGA ACCGCCAGGG CGAGACGAAA GCGACATCGC TTCCATCTTT 60

ACGACCAAGA ATCGCCTTCA GCCCTGTCTG GTGCATCCTT GGCAGAAAGT GAGGAGGRAA 120

ACACCCCAT TGTTCCTTGG C ATG GAC ACA AGT TCA GTG GGA GGA TTA GAA 171
 Met Asp Thr Ser Ser Val Gly Gly Leu Glu
 -25 -20

TTG ACT GAT CAG ACT CCT GTT TTA TTA GGG AGT ACG GCC ATG GCA ACT 219
 Leu Thr Asp Gln Thr Pro Val Leu Leu Gly Ser Thr Ala Met Ala Thr
 -15 -10 -5

AGT CTC ACG AAT GTA GGA AAC TCA TTT AGT GGT CCA GCT AAT CCT TTA 267
 Ser Leu Thr Asn Val Gly Asn Ser Phe Ser Gly Pro Ala Asn Pro Leu
 1 5 10

GTG TCT AGA TCT AAT AAG TTT CAG AAC TCG TCA GTG GAA GAT GAT GAT 315

(2) INFORMATION FOR SEO ID NO: 158:

(A) LENGTH: 244 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Kidney

(A) NAME/KEY: sig_peptide
(B) LOCATION: 92..184
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.3
seq ILLLTHVPPWILE/NP

ACACACGTCC	CGCMGTGGAT	ACTGGAGAAT	CCTTGCCACA	CACGTCTCTGC	CGTGACACT	60
GGAGAATCCT	TCTCGCCACA	CACTTCCCAC	C	ATG GAC ACT GGA GAA TCC TTC	112	
				Met Asp Thr Gly Glu Ser Phe		
				-30 -25		
TCG CCA CAC ACG TCC TGC CGT GGA CAC TGG AGA ATC CTT CTA CTC ACA	160					
Ser Pro His Thr Ser Cys Arg Gly His Trp Arg Ile Leu Leu Leu Thr						
-20 -15 -10						
CAC GTC CCA CCG TGG ATA CTG GAG AAT CCT TCT TGC CAC ACA CGT CCC	208					
His Val Pro Pro Trp Ile Leu Glu Asn Pro Ser Cys His Thr Arg Pro						
-5 1 5						
GCC GTG GAC ACT GGA GAA TCC TTC TCG CCA CAA CGG	244					
Ala Val Asp Thr Gly Glu Ser Phe Ser Pro Gln Arg						
10 15 20						

(2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 154..246
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq LVLLSVLKEPVSR/SI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

```

ATAGGACTGC TACAAAAACC CCATGTTTAC GAATTTGCCA GTGATATTGC CCCCTTCCTG    60
TGTCATCCCA ATTTATGGAT ACGTTATGGT GCCGTGGGAT TTATCACAGT GGTAGCTCGT   120
CAAATAAGTA CAGCTGATGT CTACTGTAAA CTG  ATG  CCT  TAT  CTT  GAC  CCA  TAT   174
                               Met Pro Tyr Leu Asp Pro Tyr
                               -30                      -25

ATT ACC CAA CCA ATA ATA CAG ATT GAA AGA AAA CTT GTT CTG CTC AGT     222
Ile Thr Gln Pro Ile Ile Gln Ile Glu Arg Lys Leu Val Leu Leu Ser
                    -20                      -15                      -10

GTT TTA AAG GAA CCA GTA AGT CGT TCT ATA TTT GAT TAT GCT TTG AGG     270
Val Leu Lys Glu Pro Val Ser Arg Ser Ile Phe Asp Tyr Ala Leu Arg
                    -5                      1                      5

TCT AAA GAT ATT ACT AGC TTG TTC AGA CAT CTT CAC ATG CGT CAG AAG     318
Ser Lys Asp Ile Thr Ser Leu Phe Arg His Leu His Met Arg Gln Lys
                    10                      15                      20

AAA CGA AAT GGT TCT CTT CCC GAC TGC CCT CCG CCA GAG GAT CCT GCC     366
Lys Arg Asn Gly Ser Leu Pro Asp Cys Pro Pro Pro Glu Asp Pro Ala
                    25                      30                      35                      40

ATA GCA CAG CTT CTG AAG AAG TTG CTC TCA CAG GGA ATG ACA GAG GAA     414
Ile Ala Gln Leu Leu Lys Lys Leu Leu Ser Gln Gly Met Thr Glu Glu
                    45                      50                      55

GAG GAA GAC AAA CTT CTG GCA CTG AAA GAC TTC ATG ATG                 453
Glu Glu Asp Lys Leu Leu Ala Leu Lys Asp Phe Met Met
                    60                      65

```

(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 181..267
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq VLLGSTAMATSLT/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

```

ARRAAAGCCG GGACTGGACC GAGCGGAGTK KTGCGTGTCTG CCGAAGGGGG GTKGGCCGGG      60
GGAGGKGAGG TTCGTTCCGC GGAKCCGCAG YCAGAASCGK GRACCAAGAA TCGCCTTCAG      120
CCCTGTCTKG TGCATCCTTG GCAGAAAGTG RKGAKGAAAA CACCCCCATT GTTCTTTGGC      180
ATG GAC ACA AGT TCA GTG GGA GGA TTA GAA TTG ACT GAT CAG ACT CCT      228
Met Asp Thr Ser Ser Val Gly Gly Leu Glu Leu Thr Asp Gln Thr Pro
          -25                      -20                      -15
GTT TTA TTA GGG AGT ACG GCC ATG GCA ACT AGT CTC ACG AAT GTA GGA      276
Val Leu Leu Gly Ser Thr Ala Met Ala Thr Ser Leu Thr Asn Val Gly
          -10                      -5                      1
AAC TCA TTT AGT GGT CCA GCT AAT CCT TTA GTG TCT      312
Asn Ser Phe Ser Gly Pro Ala Asn Pro Leu Val Ser
          5                      10                      15

```

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 33..116
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq FGLLDFVVQCCDS/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

ATTTTTTATG	ACATCTA	WTT	ATATTGAGTT	GC	ATG	CAT	GTT	TTG	TTC	AAC	ATA					53
					Met	His	Val	Leu	Phe	Asn	Ile					
								-25								
GTC	ACA	ACA	AAT	WRR	RAT	AAC	CAT	TTT	GGG	TTG	TTA	GAT	TTT	GTT	GTG	101
Val	Thr	Thr	Asn	Xaa	Xaa	Asn	His	Phe	Gly	Leu	Leu	Asp	Phe	Val	Val	
	-20					-15					-10					
CAG	TGT	TGT	GAT	TCA	TTA	AGA	AAC	CAT	ARG	WGG	TCA	TTT	CAG	TCA	TCT	149
Gln	Cys	Cys	Asp	Ser	Leu	Arg	Asn	His	Xaa	Xaa	Ser	Phe	Gln	Ser	Ser	
-5					1				5				10			
TAC	TTG	AGG	CTA	AAT	CAT	TCA	TGR	CAT	ACA	TGT						182
Tyr	Leu	Arg	Leu	Asn	His	Ser	Xaa	His	Thr	Cys						
			15					20								

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 150..215
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq TAYWLSFMSWAQS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

ATGTATACTG	AGGTTTCAGGA	ACTGCTGGAG	AGATGACTGG	GCACCAAGAG	GATGACAGTG	60
ACTCAGCTGG	CATCCCTTAG	CTGGTTCATG	GCAGAGCTGA	GTGGCCACTC	CTGTCTCTGA	120
CCCCAGCTTC	AGTGCTCTTT	ATCTCCTCC	ATG CCT CCT	CAG TCG TGC	TGC TCT	173
			Met Pro Pro	Gln Ser Cys	Cys Ser	
			-20		-15	

AAG ACT GCT TAC TGG CTT TCC TTC ATG TCC TGG GCA CAG AGC AGT TCT	221
Lys Thr Ala Tyr Trp Leu Ser Phe Met Ser Trp Ala Gln Ser Ser Ser	
-10 -5 1	
TTT GGT AGC AGA HTT GAG TCC ACT TCC CCC TGC ACA GAT CAC TGC TCA	269
Phe Gly Ser Arg Xaa Glu Ser Thr Ser Pro Cys Thr Asp His Cys Ser	
5 10 15	
GGA CCC AGA GAG GAG CAG CTC TGC TCC AGC AGG GTT TTC CAT TGC ATC	317
Gly Pro Arg Glu Glu Gln Leu Cys Ser Ser Arg Val Phe His Cys Ile	
20 25 30	
ACA CAC CCA AAC GGT AGG ATC CAC CGG TGG	347
Thr His Pro Asn Gly Arg Ile His Arg Trp	
35 40	

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 53..94
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq SCVFFHFLQGGLG/FG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

AACTTTCTTC AAGGCGGTTT GGGATTGGC TCCGCTGGCC GCTGTGCTGG TG ATG TCC	58
Met Ser	
TGT GTT TTC TTT CAC TTT CTT CAA GGC GGT TTG GGA TTT GGC TCC GCT	106
Cys Val Phe Phe His Phe Leu Gln Gly Gly Leu Gly Phe Gly Ser Ala	
-10 -5 1	
GGC CGC TGT GCT GGT GAC AGG	127
Gly Arg Cys Ala Gly Asp Arg	
5 10	

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 156..215
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq LILLPIWINMAQI/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

```
AAACTCGAAC TTGGTCGGGG CGCGGATCCC GAGAGGGAAA GTCATAACAA CCGCACGAGG    60
GAGTTCGACT GCGGAAC TGG AAGGCCACGC CTCCTCCCGC CTGCCCCCTC AGCCCTGTGG    120
CTGGGGGCAG AGCTCAGACT GTCTTCTGAA GATTG ATG TCT ATT TCC TTG AGC        173
                               Met Ser Ile Ser Leu Ser
                               -20                               -15

TCT TTA ATT TTG TTG CCA ATT TGG ATA AAC ATG GCA CAA ATC CAG CAG        221
Ser Leu Ile Leu Leu Pro Ile Trp Ile Asn Met Ala Gln Ile Gln Gln
                               -10                               -5                               1

GGA GGT CCA GAT GAA AAA GAA AAG ACT ACC GCA CTG AAA GAT TTA TTA        269
Gly Gly Pro Asp Glu Lys Glu Lys Thr Thr Ala Leu Lys Asp Leu Leu
                               5                               10                               15

TCT AGG ATA GAT TTG GAT GAA CTA ATG AAA AAA GAT GAA CCG CCA GGG        317
Ser Arg Ile Asp Leu Asp Glu Leu Met Lys Lys Asp Glu Pro Pro Gly
    20                25                30
```

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 50..151
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq SFCNAVVLSPVFQ/EE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

```

AAGTTATACA GAAGACTTGT AGGAAGGATG GACAAACGTT CTTAAGCCC ATG ACG GCC    58
                                   Met Thr Ala

CTT AAC CTG GTC GCT CCC TTT TCT GAT GGA GAC TCA GGC AGC GTC TCT    106
Leu Asn Leu Val Ala Pro Phe Ser Asp Gly Asp Ser Gly Ser Val Ser
-30                               -25                -20

CTA GCT TCT TTC TGC AAT GCT GTA GTA CTC TCT CCA GTA TTT CAG GAG    154
Leu Ala Ser Phe Cys Asn Ala Val Val Leu Ser Pro Val Phe Gln Glu
-15                               -10                -5                1

GAG GAG CAT TTG CTA TTT CAA AAA CGA AAA ACA AAA ACC TGG CCA CCC    202
Glu Glu His Leu Leu Phe Gln Lys Arg Lys Thr Lys Thr Trp Pro Pro
                    5                10                15

AGG                                                                205
Arg

```

(2) INFORMATION FOR SEQ ID NO: 166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 154..204
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq PVQVLGLLATCQH/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

```

AATATGTAAC CAAAAATAAA GTGTTTCAAT AGTTTATTCC TCTTTCATAT AATGGTCTAG    60

AGAGAGTGTC ATTGGGGCAA AGGGCAAAGA TACAGAGGAT CTGTTTCCCT TCTATCTTGT    120

TTTTCTGTAA TCACCTAGAG CAGTGCTACT CAA ATG TGG TCC AGA CCA GTG CAG    174
                                   Met Trp Ser Arg Pro Val Gln
                                   -15

GTC TTG GGA CTT CTT GCC ACT TGT CAG CAT GCT CCC TCT CCC TCC TTT    222
Val Leu Gly Leu Leu Ala Thr Cys Gln His Ala Pro Ser Pro Ser Phe
-10                               -5                1                5

AAA GGT GAG ACA TGT ACA GAA ATT GAG AGT GTT TAT CTG GCC CCC ATG    270

```


Lys Gly Glu Thr Cys Thr Glu Ile Glu Ser Val Tyr Leu Ala Pro Met
 10 15 20

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 125..196
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq SLNQILLFLLISC/RT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

```

TACTGTGGTA AGCACTTAGT AATGCAAAGT ATTGTTATTC TAATTATTTTC CAATAAGAAT      60
AGTGCCTTTT ATTGGGGAAA GAGTCTACTT GGCTGATCAC AACAAGAGGT TTATTTCTTC      120
CTCC ATG AGG TAC CGG TTA AGG ATT CAA ATC ACA ACA TCC CTC AAT CAG      169
  Met Arg Tyr Arg Leu Arg Ile Gln Ile Thr Thr Ser Leu Asn Gln
                -20                      -15                      -10

ATC CTG CTA TTC TTA CTG ATA AGT TGT AGG ACC TTG AGC                        208
Ile Leu Leu Phe Leu Leu Ile Ser Cys Arg Thr Leu Ser
                -5                      1

```

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 271..345

(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq VLLFFCCSPLYSP/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

ATGTAATGGA	AGCAATCATT	TTGAAAAGAG	TTAAAGTTT	TTGGTAAGTC	AAATAAGGAT	60
CAATGCTGCT	GAAAGCTGGG	ACAACACACG	GGCCCTGACC	AAATTGGGGT	TTCTTTGTCT	120
ACCTCATACC	TTCCAAATCA	AAAAATAATT	TCCCTAGTAT	TTTAATTACT	CCCCCAAATC	180
AGGAATAACT	TCCTCACTGT	GCTGATTTTG	GTTCTTTTAA	AATAAGGTGG	TAATTTGAAG	240
GTAATAGTTA	AACCAGTCAT	AGATTATTCT	ATG CCA TTC TTT TCA AAT CAG CCC			294
			Met Pro Phe Phe Ser Asn Gln Pro			
			-25		-20	
ACT CAG GTG TCA GTC CTA CTT TTC TTT TGT TGT AGT CCT CTT TAT TCT						342
Thr Gln Val Ser Val Leu Leu Phe Phe Cys Cys Ser Pro Leu Tyr Ser						
	-15		-10		-5	
CCT TTG TTT CTG CTC CAV CTC ATC CCC CAC CAG						375
Pro Leu Phe Leu Leu Xaa Leu Ile Pro His Gln						
1		5			10	

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 376 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 32..163
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.1
seq IAVGLTCQHVSHA/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

GCTGCGGCCC GGCCCGGCGG GTAAATAACA G ATG CGG GTG AAA GAT CCA ACT 52
Met Arg Val Lys Asp Pro Thr
-40

AAA GCT TTA CCT GAG AAA GCC AAA AGA AGT AAA AGG CCT ACT GTA CCT 100
Lys Ala Leu Pro Glu Lys Ala Lys Arg Ser Lys Arg Pro Thr Val Pro
-35 -30 -25

CAT GAT GAA GAC TCT TCA GAT GAT ATT GCT GTA GGT TTA ACT TGC CAA	148
His Asp Glu Asp Ser Ser Asp Asp Ile Ala Val Gly Leu Thr Cys Gln	
-20 -15 -10	
CAT GTA AGT CAT GCT ATC AGC GTG AAT CAT GTA AAG AGA GCA ATA GCT	196
His Val Ser His Ala Ile Ser Val Asn His Val Lys Arg Ala Ile Ala	
-5 1 5 10	
GAG AAT CTG TGG TCA GTT TGC TCA GAA TGT TTA AAA GAA AGA AGA TTC	244
Glu Asn Leu Trp Ser Val Cys Ser Glu Cys Leu Lys Glu Arg Arg Phe	
15 20 25	
TAT GAT GGG CAG CTA GTA CTT ACT TCT GAT ATT TGG TTG TGC CTC AAG	292
Tyr Asp Gly Gln Leu Val Leu Thr Ser Asp Ile Trp Leu Cys Leu Lys	
30 35 40	
TGT GGC TTC CAG GGA TGT GGT AAA AAC TCA GAA AGC CAA CAT TCA TTG	340
Cys Gly Phe Gln Gly Cys Gly Lys Asn Ser Glu Ser Gln His Ser Leu	
45 50 55	
AAG CAC TTT AAG AGT TCC AGA ACA GAG CCC CTC AGG	376
Lys His Phe Lys Ser Ser Arg Thr Glu Pro Leu Arg	
60 65 70	

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 9..140
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq GTYLTSSSPQCQL/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

ACTTTAAT ATG GTG TCC TTG GGT TAT TAT TTA ATA TTT GTC CTA TAT CTT	50
Met Val Ser Leu Gly Tyr Tyr Leu Ile Phe Val Leu Tyr Leu	
-40 -35	
TGG CTT TGT TTC ATG CAA ATT AGT GAA GAG AAG TTA ATA GAG GAA CAC	98
Trp Leu Cys Phe Met Gln Ile Ser Glu Glu Lys Leu Ile Glu Glu His	
-30 -25 -20 -15	
ACA GGT ACA TAT TTA ACC TCC AGT TCA CCC CTC TGC CAG CTC CAG CCC	146
Thr Gly Thr Tyr Leu Thr Ser Ser Ser Pro Leu Cys Gln Leu Gln Pro	

CCA GGG
Pro Gly

152

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 128..232
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq VLCCLLIATPTFF/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

```

ATATTATTAA ACTTTTATT TTGAGGTTAG TGTGGATTGA AATACACTTC CAACAATTAA      60
CACAAAGGTC CCCTGTGTCC TTTACCCAGT TTTCCACAAT GGTAACATCT TACAAAAC TG      120
GAGTACA ATG TCA CTC ACA TCC AGG RTA MYA ATW ATG GWT ACA ATC AAG      169
    Met Ser Leu Thr Ser Arg Xaa Xaa Ile Met Xaa Thr Ile Lys
    -35                      -30                      -25
ATA CAG AAT ATT TCT ATT ACA AAG GTC TTG TGT TGC CTT CTT ATA GCA      217
Ile Gln Asn Ile Ser Ile Thr Lys Val Leu Cys Cys Leu Leu Ile Ala
    -20                      -15                      -10
ACA CCT ACT TTC TTC CTA CTC CTT CCC TCA TCC ATT CCA CGG      259
Thr Pro Thr Phe Phe Leu Leu Pro Ser Ser Ile Pro Arg
    -5                      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 137..190
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.1
 seq AGVVSTSVAAAVA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

```

AAGCGCAACC GGAAGTAGCC TTCTGGGGGC CGGCTTCCTT TATCTCTGGC GGCCTTGTAG    60
TCGTCTCCGA GACTCCCCAC CCCTCCTTCC CTCTTGACCC CCTAGGTTTG ATTGCCCTTT    120
CCCCGAAACA ACTATC ATG ARC GCC GAG GCT GCC GGT GTT GTC TCC ACC TCG    172
          Met Xaa Ala Glu Ala Ala Gly Val Val Ser Thr Ser
                    -15                               -10

GTG GCC GCG GCT GTT GCT GCT GTC GCT GCT CCT GCT GGG GCC GGG    217
Val Ala Ala Val Ala Ala Val Ala Ala Pro Ala Gly Ala Gly
      -5              1              5
  
```

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 196 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 101..145
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4
 seq IMSSCLALTYTNS/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

```

TTGGTATCTG GAGTGTGTGA GTGTGTTTGT ATTTGCTTAT AAATAAGTAT TATAGATAAA    60
GATAAACTTC ATAAAGAGTG GATATTTTGG GGAAAATTTT ATG TGG ATA ATG TCA    115
          Met Trp Ile Met Ser
                    -15

TCC TGT CTG GCA TTG ACA TAC ACA AAT TCA ATC TCA CAT AGT CTT TGC    163
Ser Cys Leu Ala Leu Thr Tyr Thr Asn Ser Ile Ser His Ser Leu Cys
-10              -5              1              5
  
```

CTT GAG AGA GCG TAC AGT CTA TTC AAA GTT GAC
 Leu Glu Arg Ala Tyr Ser Leu Phe Lys Val Asp
 10 15

196

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 65..124
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq SNALVLVTRGSSS/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

ACAGTGTGGC TCGGTTGAAT AGGAGAGCTT TAACTGCATT CTCTGTGAG AATGCAGTBG	60
AAGA ATG CCA AGA GGA GTG TAC AAT TCA AAT GCG TTA GTG CTT GTA ACA	109
Met Pro Arg Gly Val Tyr Asn Ser Asn Ala Leu Val Leu Val Thr	
-20 -15 -10	
CGT GGT TCC AGT TCT CTC CCT CTT GGC TTG TAT GGT ATA AAT TGT GTA	157
Arg Gly Ser Ser Ser Leu Pro Leu Gly Leu Tyr Gly Ile Asn Cys Val	
-5 1 5 10	
CAG GTA ATT AAG TTA TTT TAT AGA GGC CAT CTC CAC TGG GAA ACT TTG	205
Gln Val Ile Lys Leu Phe Tyr Arg Gly His Leu His Trp Glu Thr Leu	
15 20 25	
CTG CCA TCG	214
Leu Pro Ser	
30	

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 210..341
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq FLLPCVHPFSVIA/VY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

```

AATTTATGAT AGGAAATGAT TGATCAAGTG TCACACAGCT GATTATCAGG TCTCAGTCTA    60
ATATTTATTC CTTATTGGTC TCTGCTTAAC TTCAAGTAGG TTATAGATTC CTTAATGGAC    120
TGATAGTTTA TGTCTTATAG CTTTACCTTT CAGGCGCTTA GTTTCATATT GGGAACATGA    180
CAAGTGAATA ATAAATACAT GATAGCTCT ATG ATT GAA CCC TGT GAG AAA ATG      233
                               Met Ile Glu Pro Cys Glu Lys Met
                               -40

AAG CAT TAT GAT ATG AAT TGG TTT CTG TGT ATG TAT GAG TGT TTT TTT      281
Lys His Tyr Asp Met Asn Trp Phe Leu Cys Met Tyr Glu Cys Phe Phe
-35                               -30                               -25

TTY CAT CTT TTG GAA ACA GAA TTT CTG CTC CCC TGT GTA CAC CCT TTC      329
Phe His Leu Leu Glu Thr Glu Phe Leu Leu Pro Cys Val His Pro Phe
-20                               -15                               -10                               -5

TCT GTA ATT GCA GTG TAT GTT TTT
Ser Val Ile Ala Val Tyr Val Phe
1

```

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 134..298
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq AALCGISLSQXFP/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

```

AGCCTCCGCC TTTGCCTTCG CAGCCGCCTC CAGGGCAATT TGCATATTTC TCCAAAGAAC    60
CATCCAGAAC CTGAGCAGCC TGTCTTCAGA CAGAGATAGG CCCACGGCTG TTTCTTGAAA    120
TCTGGCGCTG GGA ATG GCC ATG TGG AAC AGG CCA TGC CAG ARG CTG CCT    169
          Met Ala Met Trp Asn Arg Pro Cys Gln Xaa Leu Pro
          -55                    -50                    -45

CAG CAG CCT CTG GTA GCT GAG CCC ACT GCA GAG GGG GAG CCA CAC CTG    217
Gln Gln Pro Leu Val Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu
          -40                    -35                    -30

CCC ACG GGC CGG GAG CTG ACT GAG GCC AAC CGC TTC GCC TAT GCT GCC    265
Pro Thr Gly Arg Glu Leu Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala
          -25                    -20                    -15

CTC TGT GGC ATC TCC CTG TCC CAG TKA TTT CCT GAA CCG GGG    307
Leu Cys Gly Ile Ser Leu Ser Gln Xaa Phe Pro Glu Pro Gly
          -10                    -5                    1

```

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 130..180
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq CLLVSYAVDSAAG/RF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

```

ATTGTCAAAA AGACATCAAA CTCAACTTCT GGGAAGACAG ATTTTAAATA CACATACTTG    60
GCTAATACTC ACAAACATAT CTAAAGTTTT GGCAAAATTA TGAGGGTGAT GGGTKGGTAC    120
TAACCTGGC ATG GAG CAG GTG TGT CTT TTG GTT TCT TAT GCA GTT GAC TCT    171
          Met Glu Gln Val Cys Leu Leu Val Ser Tyr Ala Val Asp Ser
          -15                    -10                    -5

GCT GCA GGG AGA TTC GGG    189
Ala Ala Gly Arg Phe Gly
          1

```


(2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 20..103
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq ATLRCWASTPVSG/RL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

ACAAAGAGGC AGCTCCGGA ATG AGA AAG ATA AGC CAC TGC CTC CAC TGC TGG	52
Met Arg Lys Ile Ser His Cys Leu His Cys Trp	
-25 -20	
CCC GAG TCG GGG GCA ACA TTG AGG TGC TGG GCT TCA ACA CCC GTC AGC	100
Pro Glu Ser Gly Ala Thr Leu Arg Cys Trp Ala Ser Thr Pro Val Ser	
-15 -10 -5	
GGA AGG CTT TCC TCA ATG GCT GTK RWG SSG CKG GGG GAA AKG CCA CCA	148
Gly Arg Leu Ser Ser Met Ala Val Xaa Xaa Xaa Gly Glu Xaa Pro Pro	
1 5 10 15	
CAG GAT GCC TTC ACC ACA CAG TGG CTG GTG CGG GAC CTG AGG GGC AAG	196
Gln Asp Ala Phe Thr Thr Gln Trp Leu Val Arg Asp Leu Arg Gly Lys	
20 25 30	
ACT GAG AAG GAG TTT AAG GCC TAT GTG TCT TTG TTC ATG CGC CAT CTG	244
Thr Glu Lys Glu Phe Lys Ala Tyr Val Ser Leu Phe Met Arg His Leu	
35 40 45	
TGT GAG CCT GGG GCA GAC GGC TCT GAA ACC TTT GCC GAT GGG GTC CCT	292
Cys Glu Pro Gly Ala Asp Gly Ser Glu Thr Phe Ala Asp Gly Val Pro	
50 55 60	
CGG GAG GGA CTG AGT CGC CAG CAG GTG TTG ACC CGC ATT GGA GTC ATG	340
Arg Glu Gly Leu Ser Arg Gln Gln Val Leu Thr Arg Ile Gly Val Met	
65 70 75	
TCT CTC GTC AAA AAG AAG GGG CAG	364
Ser Leu Val Lys Lys Lys Gly Gln	
80 85	

(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 172..237
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq LLHPCGSITLTSS/ST

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

```

AAAATTTTTT TAGCCTCTAA CATGAAAGGG TCTCTTCATT GTTCTCATTT GTCTTACCCG    60
CCATCCAGTG TTAAGCAGTA TGTTAAAGAG CTTCTTCTTT ACAACTTTTC CCCTCACATT    120
ATTTYCTAC ATGCAGCAAC TTCTTTAACC AAGTTGTTTG ATTAGGAGTA A ATG TGC    177
                                     Met Cys
ATA AAC GAT CAT ATT ATT AAG CTT CTG CAC CCA TGT GGC AGC ATC ACT    225
Ile Asn Asp His Ile Ile Lys Leu Leu His Pro Cys Gly Ser Ile Thr
-20                      -15                      -10                      -5

TTA ACT TCT TCC TCA ACC ACA CGG                                249
Leu Thr Ser Ser Ser Thr Thr Arg
      1

```

(2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 135..185
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4
seq VALQCGLTIPALX/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

```

AGAAGGGGTG TCAAACCTCCA ATGGAAAAGG TTTAGGAAAA GACCTTTTAC AAATCCAAAG   60
ATGTTTCACA GTGGGCGAGG CTGGTGTGGC GACAGTAGTG GCCCACATGG CTGGGTTGGG   120
AGCCAGCTCT GCCC ATG AGG TGC CGT GTG GCT TTG CAG TGT GGC CTC ACA   170
          Met Arg Cys Arg Val Ala Leu Gln Cys Gly Leu Thr
                   -15                               -10
ATC CCA GCT TTG TNT CTT CCC CAG GGA GAT GAG GCT GGT GAT GCT CAA   218
Ile Pro Ala Leu Xaa Leu Pro Gln Gly Asp Glu Ala Gly Asp Ala Gln
-5              1              5              10
GAT CTC AGA GGC CCT GCC CAG GCT GAG TAT CTG TAT ATA ATA TCC CCC   266
Asp Leu Arg Gly Pro Ala Gln Ala Glu Tyr Leu Tyr Ile Ile Ser Pro
          15              20              25
TCG
Ser
269

```

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 88..366
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq LTSAFLWLPRLHI/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

```

ATATACTCA GTTTTCTGTT GTCTTTAGCT ACTGATGCAA ATGTGAAGAA TGAAAGTCTT   60
TCATCTGTGC AGCAGCTTGG CATTAAA ATG ACT GTC AGG TAT GGC AAA TTC CTC   114
          Met Thr Val Arg Tyr Gly Lys Phe Leu
                   -90                               -85
AGT CTC TTA AAA GAT GGT GCA GAA AAT GAT CTT ACC TGG GTT TTA AAG   162
Ser Leu Leu Lys Asp Gly Ala Glu Asn Asp Leu Thr Trp Val Leu Lys
          -80              -75              -70

```

CAT TGT GAG AGA TTC CTG AAA CAG CAG CAA ACT TCC ATA AAA TCT TCT	210
His Cys Glu Arg Phe Leu Lys Gln Gln Gln Thr Ser Ile Lys Ser Ser	
-65 -60 -55	
CTT CTC TGC CTG CAA GGG AAT TAT GCT GGC CAT GAC TGG TTT GTA TCT	258
Leu Leu Cys Leu Gln Gly Asn Tyr Ala Gly His Asp Trp Phe Val Ser	
-50 -45 -40	
TCT CTG TTC ATG ATA ATG TTG GGA GAC AAA GAA AAA ACA TTC CAA TTT	306
Ser Leu Phe Met Ile Met Leu Gly Asp Lys Glu Lys Thr Phe Gln Phe	
-35 -30 -25	
CTT CAT CAA TTC TCC AGG CTT CTG ACT TCT GCT TTT CTT TGG TTG CCA	354
Leu His Gln Phe Ser Arg Leu Leu Thr Ser Ala Phe Leu Trp Leu Pro	
-20 -15 -10 -5	
AGG CTA CAT ATT TCT GTA AGA CTT CAA TCT GTT TTT AAA GGA GGG TTT	402
Arg Leu His Ile Ser Val Arg Leu Gln Ser Val Phe Lys Gly Gly Phe	
1 5 10	
GAM ATT TTA AGA ACA TTA TAC TTA CAT TCA MCG GGA CGG	441
Xaa Ile Leu Arg Thr Leu Tyr Leu His Ser Xaa Gly Arg	
15 20 25	

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 160..219
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq FFWVVLFSAGCKV/IT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

AACAGAGCCA CAGAATGCTG AGCAGTCAAC AGCATTTCTT GTTCCAAGAT CACCCTTCTG	60
AGTACCTCTC TGGCTGCCAA ATTGCCAGGG CCTTCACAGT TTGATTCCAT TTCTCAGCTC	120
CAAGCATTAG GTAAACCCAC CAAGCAATCC TAGCCTGTG ATG GCG TTT GAC GTC	174
Met Ala Phe Asp Val	
-20	
AGC TGC TTC TTT TGG GTG GTG CTG TTT TCT GCC GGC TGT AAA GTC ATC	222

Ser Cys Phe Phe Trp Val Val Leu Phe Ser Ala Gly Cys Lys Val Ile
 -15 -10 -5 1
 ACC TCC TGG GAT CAG ATG TGC ATT GAG AAA GAA GCC ACA 261
 Thr Ser Trp Asp Gln Met Cys Ile Glu Lys Glu Ala Thr
 5 10

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 167..232
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq HLSSTTSPPWTHA/AI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

AAAAACGCCT TGAGGATAAG GAAGGAGAAT CAGCAAGTCC CGAGTTCCTA CGGTGTGTCA 60
 GCATCGTGCT CCCACTCCCG GGAGAGAGGC ATTATCTTCA GTTTACAAAA GGGGAAAACA 120
 GGTCTGGGGT TTCCAGAGTC CGCGGTTTTG CTAAGAAGCC GCAGTG ATG TTG ACG 175
 Met Leu Thr
 -20
 CGG CTG GTC CTC AGT GCA CAC CTG AGT AGC ACG ACC TCT CCG CCC TGG 223
 Arg Leu Val Leu Ser Ala His Leu Ser Ser Thr Thr Ser Pro Pro Trp
 -15 -10 -5
 ACG CAC GCT GCC ATC AGC TGG GAG CTG GAC AAC GTG CTG ATG CCT AGT 271
 Thr His Ala Ala Ile Ser Trp Glu Leu Asp Asn Val Leu Met Pro Ser
 1 5 10
 CCC AGA ATC TGG CCC CTG 289
 Pro Arg Ile Trp Pro Leu
 15

(2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 326..445
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq CVNLLLGFEFVIS/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

```

ATAAACTTA GGGGGAAGAT TTGCCTCTCA CTTTTTTTCT TGGAAAATGT GGGCAGCAAT   60
TTTAAAGAGA ACATGAAAAT GGAGTAGGTT GAAACCAACA TTCAGAACTT CCTTTCATGG   120
ATTGAAACTT AAAGCTGAGG GAGGKTTTRA GGGTGGARKT RAGGAAGGGC TAGAAGATAG   180
CAAATTTTCA AGTCATATCA GAGAATATGA ACTGTCAGTG TTTCCAATGT TTCTCTTGGC   240
TCTGCACAGC ACTTCCAAGC CCTTTTGCTC ACTGTTTTGC TTCTGCCACA CCTAGGAGAA   300
GATTCAGAGC TTGCTGAGGC AAAAC ATG CGA TAT TTC CAA GGG CCT TCC CCC   352
                        Met Arg Tyr Phe Gln Gly Pro Ser Pro
                        -40                        -35

TAT TCT GAA ATA GAA ATT GAG CTT TGT GAT CAT GTG TAT TCA TTC CAA   400
Tyr Ser Glu Ile Glu Ile Glu Leu Cys Asp His Val Tyr Ser Phe Gln
-30                        -25                        -20

GGT CTA TGT GTT AAC CTT TTG CTA GGA TTT GAA CCT GTT ATT AGT AGG   448
Gly Leu Cys Val Asn Leu Leu Leu Gly Phe Glu Pro Val Ile Ser Arg
-15                        -10                        -5                        1

AGC CGR MGC AGT TCA CTT GCT GTT GAG TCT   478
Ser Arg Xaa Ser Ser Leu Ala Val Glu Ser
                    5                        10

```

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 48..170
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.9
 seq LASLECYVPSTNQ/WQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

ACTGCAGATA CGATCCCCGC TTCAACACCT GGATACACCT GGCCAGS	ATG AAN HAG	56
	Met Xaa Xaa	
	-40	
AAG CGC ACG CAC TKV VNS STG AGC GTG TTC AAC GGG CTC GTG TAC GCC		104
Lys Arg Thr His Xaa Xaa Xaa Ser Val Phe Asn Gly Leu Val Tyr Ala		
-35	-30	-25
GCG GGC GGC CGC AAC GCA GAA GGA AGC CTG GCC TCG CTG GAG TGC TAC		152
Ala Gly Gly Arg Asn Ala Glu Gly Ser Leu Ala Ser Leu Glu Cys Tyr		
-20	-15	-10
GTG CCC TCC ACC AAT CAG TGG CAG CCG AAG HHN SCC CTG GAG GTG GCG		200
Val Pro Ser Thr Asn Gln Trp Gln Pro Lys Xaa Xaa Leu Glu Val Ala		
-5	1	5
		10
CGC TGC TGC CAC GCT AGC GCG GTC GCC GAC GGC CGC GTG CTG GTG ACC		248
Arg Cys Cys His Ala Ser Ala Val Ala Asp Gly Arg Val Leu Val Thr		
15	20	25
GGA GGC TTG		257
Gly Gly Leu		

(2) INFORMATION FOR SEQ ID NO: 186:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 249..362
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.9
 seq LLFFHLLLNDFFT/FY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

```

ACATCCAGCT CTGGTAGTTT AGGCTCAATC TTACGGTGTA ATTATACAGA ATAATTAGAG    60
GCAGCTGTAT CCTTGTTTCT GATTTTAAAA TCTGRATGTT TCTYCAATTC TTTGTGTACT    120
CTCCCTTCAT TTGGTACATA TAGAAGTCTT CTTATGTGTT ATTAAAGTCT TCTAAGATAG    180
TATTCTGGTC ATTGAGAGACA CCAAAAATCT ATGGGCACAG TCCTGTTTCT GTTTCTTTTG    240
CCAATAGA ATG TTC CTT AAG GTT CAG TCA CAG TCC TTT TAC DTC CCT TAC    290
      Met Phe Leu Lys Val Gln Ser Gln Ser Phe Tyr Xaa Pro Tyr
              -35                      -30                      -25

AGA GAT TGT TTA AAT TTC CAC AAA AGC ACG TAT TTA CTC TTC TTT CAC    338
Arg Asp Cys Leu Asn Phe His Lys Ser Thr Tyr Leu Leu Phe Phe His
              -20                      -15                      -10

TTG TTA CTA AAT GAC TTC TTC ACA TTT TAC NTT GCT AAA    377
Leu Leu Leu Asn Asp Phe Phe Thr Phe Tyr Xaa Ala Lys
              -5                      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 119..199
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq WIILIIYTFQCNS/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

```

CAGAATGTTC TTTGCTGCCT CGCTTACATG GCAAACTCA CAAACCACCT ATACAATCCA    60
AAAGAGGGGA AACAGCTCAT CTCATATTAA TTATGGTCCA TTTCBATGAT AGGATATT    118
ATG CAA CCA TTA AAA ATC ATA TTT TAT CTG AGT GTT AGT ATA TGG ATT    166
Met Gln Pro Leu Lys Ile Ile Phe Tyr Leu Ser Val Ser Ile Trp Ile
      -25                      -20                      -15

ATT TTA ATT ATT TAT ACT TTT CAG TGT AAT TCT TCT CTG AGC ATA CTA    214
Ile Leu Ile Ile Tyr Thr Phe Gln Cys Asn Ser Ser Leu Ser Ile Leu
      -10                      -5                      1                      5

CTT TTG GAG TTA    226
Leu Leu Glu Leu

```


(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 10..66
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq RVAACTAAAPLQA/HG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

```

AAGTGATGG ATG ATG AGA ACG ACA GCG AGA GTC GCT GCG TGT ACT GCT GCA   51
      Met Met Arg Thr Thr Ala Arg Val Ala Ala Cys Thr Ala Ala
                -15                      -10

GCC CCA TTG CAA GCC CAC GGT GCA GRC ATT CAG CAG GRT CCA GAC AGS   99
Ala Pro Leu Gln Ala His Gly Ala Xaa Ile Gln Gln Xaa Pro Asp Xaa
-5              1              5              10

CTC TGS TCT RGA AGG CTC AGC AGA GRR GGR CTT TCT GCA GGG CGR CTG   147
Leu Xaa Ser Xaa Arg Leu Ser Arg Xaa Gly Leu Ser Ala Gly Arg Leu
      15              20              25

CAC CAR AGC GAA ACA GAA GCT GAA CTG GAR GCC CCG GGT CGC GCG   192
His Gln Ser Glu Thr Glu Ala Glu Leu Glu Ala Pro Gly Arg Ala
      30              35              40

```

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: 140..241
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.8
 seq RWASSCLHPSARS/SN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

```

AASCCCAASG TGCTGCCGTT GCCCGTACAA CTCGGACTTG CTGTTGCTCG AGCCGCGTCT    60
GCACGGGTCT CGGACCGAGC GGAGTCCMAG CCTCGGTCCC GGAGCCCACC TTCGCCTCGC    120
CCTTGCCCAG CCTGCGGTG ATG GAG GCG GCC ACC ACA CTG CAC CCA GGC CCG    172
                Met Glu Ala Ala Thr Thr Leu His Pro Gly Pro
                -30                                -25

CGC CCG GCG CTG CCC CTC GGG GCC CGG GCC CGC TGG GCG AGT TCC TGC    220
Arg Pro Ala Leu Pro Leu Gly Ala Arg Ala Arg Trp Ala Ser Ser Cys
                -20                                -15                                -10

CTC CAC CCG AGT GCC CGG TCT TCG AAC CCA GCT GGG AAG AGT TCG CGG    268
Leu His Pro Ser Ala Arg Ser Ser Asn Pro Ala Gly Lys Ser Ser Arg
                -5                                1                                5

ACC CCT                                                                274
Thr Pro
10
  
```

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 196 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 92..178
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.8
 seq LCPVIFFPSNCWK/EY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

```

AAGAAAGGAC ATTTTTTTTT TCTTGTAATA ACTAGGCTGG ATTYCCAAA TTGTTTGAGT    60
GGCCCGTGCC CCTCTTAATG CTTCTGTAAG A ATG CAA GGT GTC AGG GGA CCT    112
                Met Gln Gly Val Arg Gly Pro
                -25

GTG TCC TTT TCC TGG AGC ACA ACC ATG TTG TGT CCT GTT ATA TTC TTT    160
  
```

Val Ser Phe Ser Trp Ser Thr Thr Met Leu Cys Pro Val Ile Phe Phe
-20 -15 -10

CCA TCC AAC TGT TGG AAA GAA TAT AAC AGG ACA CAG 196
Pro Ser Asn Cys Trp Lys Glu Tyr Asn Arg Thr Gln
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 177..230
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq FXLLFXXFXFFRO/XG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

ACAAAGTCTGT	CCTCCCTAGG	CTGGCAGCTC	TGTCAGCACACC	CAGGTTTGTA	GAATAGTTGT		60
TAAAACAGGT	CATTCTGTTG	CCAAGTAATT	ACGGGGGCCCTT	GSACTCAGTA	ACCTTCCCCA		120
CGAAGCAGGC	CGTAGTGTGC	TTACTGCTCT	CCCTTGSCTT	TCCATCCCCT	ACTTTG ATG		179
					Met		
TKG GRR TTT	TCT TTC YTT	TTA CTT TTC	YTT TAW TTT	CYT TTT TTC	CGC		227
Xaa Xaa Phe	Ser Phe Xaa	Leu Leu Phe	Xaa Xaa Phe	Xaa Phe Phe	Arg		
-15		-10		-5			
CAG KCT GGG							236
Gln Xaa Gly							
1							

(2) INFORMATION FOR SEQ ID NO: 192:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 359..427
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq SVRLLEFRFSVIMA/SE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

```

ACACTGTGAA ATGCAATTGT GCCTTGAATA AGAAGGTACC TAGAAGCCAA ATTAAAGTAA    60
TAATGACTTC TTATTGGCTT TGATTTTTCa TTGCAGTATA TGGGAATTGT ACAGCAGGAA   120
ATGCTTATCA TTAATTTCTG ATGTTTTTTT AAGCACAACt CGAAACATTT CGATCATACA   180
TACATAGCAG TAGAGATCTG TGCCCTTCAG GTACATTGWA TCTGACCATC AGTTTATATA   240
TGTCATTGAA TTTTAAGAAT ACTCATGTTA ATAATAGTCA TCTATCCTTG CATTTTGAAA   300
CTGTTCTAAT CTTAGTGAAC TTGAATTGGA TTTCTGGGTA AAAGAATGTG TTTCTTTT    358
ATG TTG CTT CTG TCC GAA GCC TTG TCA GAA TCT GTC AGA CTC TTG TTT    406
Met Leu Leu Leu Ser Glu Ala Leu Ser Glu Ser Val Arg Leu Leu Phe
      -20                      -15                      -10

AGG TTT AGT GTG ATC ATG GCG TCA GAG AAG CAA AGC TTT CAA ATA        451
Arg Phe Ser Val Ile Met Ala Ser Glu Lys Gln Ser Phe Gln Ile
      -5                      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 319..369
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq SLPCTTAFPLLSS/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

```

ATTCTTCTCT GGTTACCTCT ATCTACCCCC GAGTCAACAA GCCCTGCCTG ATTACGCAGC    60
AGCAGTTTCTT CCTGGAGAGT ATATGCCCTT CCCTACCAGA GTGGCTGTGC TCTGTGGACC    120
AACGGCATT TT GTGCCGTGGC TGGTGTTC ACCATTCCAG TGGGTTGGCT GCAGAGTTAT    180
CCTTTGTGGG TGGGAGAGAG CACCAGGCCT CAGGAATCTC CCTGCTGGTC CCAGCCTCCA    240
TCTCCTCCTC CCCAACCTG AACCTCTCCC GCAACCTGCA CCTCCCCCGA GAAGCCAGCC    300
ACAGAGGCAG AGAGCATC ATG GCT CTT ATC AGC CTG CCA TGC ACG ACA GCT    351
                Met Ala Leu Ile Ser Leu Pro Cys Thr Thr Ala
                  -15                               -10
TTC CCT TTA CTG TCC AGC AAG GTT TCC CAG CTT CTC TTG CCC CTC AGC    399
Phe Pro Leu Leu Ser Ser Lys Val Ser Gln Leu Leu Leu Pro Leu Ser
   -5                      1                      5                      10

```

(2) INFORMATION FOR SEQ ID NO: 194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 83..193
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq RVVALPLVRATCT/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

```

AGTGGAGAGT CGAGCCTGGG GTCGGCGGAG ACWGCTGGTG TCTGAAGCCG CTCGCGCCCA    60
GGGTGACCCT GTTTGCAGCA CG ATG TCT GAA GAA GAG GCG GCT CAG ATC CCC    112
                Met Ser Glu Glu Glu Ala Ala Gln Ile Pro
                  -35                               -30
AGA TCC AGT GTG TGG GAG CAG GAC CAG CAG AAC GTG GTG CAG CGT GTG    160
Arg Ser Ser Val Trp Glu Gln Asp Gln Gln Asn Val Val Gln Arg Val
   -25                      -20                      -15
GTG GCT CTG CCC CTG GTC AGG GCC ACG TGC ACC GCG GTC TGC GAT GTT    208
Val Ala Leu Pro Leu Val Arg Ala Thr Cys Thr Ala Val Cys Asp Val
   -10                      -5                      1                      5
TAC AGT GCA GCC AAG GAC AGG CAC CCG CTG CTG GGC TCC GCC TGG    253
Iyr Ser Ala Ala Lys Asp Arg His Pro Leu Leu Gly Ser Ala Trp

```

(2) INFORMATION FOR SEQ ID NO: 195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 8..223
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq LAELTVDPQGALA/IR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

AAAAAAG ATG GCG GCG GCG GCG GCA GCT GGT GCG GCC TCC GGG CTG CCG	49
Met Ala Ala Ala Ala Ala Ala Gly Ala Ala Ser Gly Leu Pro	
-70 -65 -60	
GGT CCA GTG GCA CAA GGA TTA AAG GAA GCG TTA GTG GAT ACG CTC ACC	97
Gly Pro Val Ala Gln Gly Leu Lys Glu Ala Leu Val Asp Thr Leu Thr	
-55 -50 -45	
GGG ATC CTA TCC CCA GTA CAG GAG GTG CGG GCG GCT GCT GAA GAA CAG	145
Gly Ile Leu Ser Pro Val Gln Glu Val Arg Ala Ala Ala Glu Glu Gln	
-40 -35 -30	
ATT AAG GTG CTG GAG GTG ACG GAG GAA TTT GGT GTT CAC TTG GCA GAA	193
Ile Lys Val Leu Glu Val Thr Glu Glu Phe Gly Val His Leu Ala Glu	
-25 -20 -15	
CTG ACT GTA GAT CCC CAG GGG GCA CTG GCA ATC CGT CAG CTG GCA TCA	241
Leu Thr Val Asp Pro Gln Gly Ala Leu Ala Ile Arg Gln Leu Ala Ser	
-10 -5 1 5	
GTC ATC TTG AAA CAA TAT GTG GAG ACT CAC TGG TGT GCC CAA TCA GAG	289
Val Ile Leu Lys Gln Tyr Val Glu Thr His Trp Cys Ala Gln Ser Glu	
10 15 20	
AAA TTT AGG	298
Lys Phe Arg	
25	

(2) INFORMATION FOR SEQ ID NO: 196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 114..464
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq XXXXYLNFCPVCYC/FS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

GTGAATTTCGC	CAGCGGGAGC	GCGCTCGCGG	WCCGCGCGTT	CTCCGCTTTC	CCGGCTCCGT	60	
CGCTGACGCG	TCGTAGASTT	GGSVWGC	GGG	AAGGCAACGG	CAGCGGGATC	GGG ATG	116
						Met	
AAC AGC GGC GGC GGC TTC GGT TTG GGC TTA GGC TTC GGC CTC ACC CCC	164						
Asn Ser Gly Gly Gly Phe Gly Leu Gly Leu Gly Phe Gly Leu Thr Pro							
-115 -110 -105							
ACG TCG GTG ATT CAG GTG ACG AAT CTG TCG TCG GCG GTG ACC AGC GAG	212						
Thr Ser Val Ile Gln Val Thr Asn Leu Ser Ser Ala Val Thr Ser Glu							
-100 -95 -90 -85							
CAG ATG CGG ACG CTT TTT TCC TTC CTA GGA GAA ATC GAG GAG CTG CGG	260						
Gln Met Arg Thr Leu Phe Ser Phe Leu Gly Glu Ile Glu Glu Leu Arg							
-80 -75 -70							
CTC TAC CCC CCG GAC AAC GCA CCT CTT GCT TTT TCC TCB DRA GTA TGT	308						
Leu Tyr Pro Pro Asp Asn Ala Pro Leu Ala Phe Ser Ser Xaa Val Cys							
-65 -60 -55							
TAT GTT AAG TTT CGT GAT CCA TCA AGT GTT GGA GTG GCC CAG CAT CTA	356						
Tyr Val Lys Phe Arg Asp Pro Ser Ser Val Gly Val Ala Gln His Leu							
-50 -45 -40							
ACT AAC ACG GTT TTT ATT GAC AGA GST CTG RAT AGT TGT TCC TTG TGC	404						
Thr Asn Thr Val Phe Ile Asp Arg Xaa Leu Xaa Ser Cys Ser Leu Cys							
-35 -30 -25							
AGA AGG TTG GTA TCT CGC TTT KTT TGN HBT TAT TTG AAT TTC TGT CCT	452						
Arg Arg Leu Val Ser Arg Phe Xaa Xaa Xaa Tyr Leu Asn Phe Cys Pro							
-20 -15 -10 -5							
GTC TGT TAT TGC TTT AGC TTT CCT AGA GAT TGG CAA GTA GAC AGT ACT	500						
Val Cys Tyr Cys Phe Ser Phe Pro Arg Asp Trp Gln Val Asp Ser Thr							
1 5 10							
CTC	503						

Leu

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 47..85
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq MIEMLIFLDCVLS/SK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

ATTAACAAAG AGCAAGTTTA ACCTGAGTGG TCAACTTTTG CAGCAG ATG ATT GAR	55
Met Ile Glu	
ATG CTA ATA TTT CTA GAC TGT GTC CTG TCT TCC AAA GAT ACA ATA ACC	103
Met Leu Ile Phe Leu Asp Cys Val Leu Ser Ser Lys Asp Thr Ile Thr	
-10 -5 1 5	
ATG TTT GTG AAG TTC ATA CCT ATT TTT CCT TTT CCT TTG CAG TTT TAT	151
Met Phe Val Lys Phe Ile Pro Ile Phe Pro Phe Pro Leu Gln Phe Tyr	
10 15 20	
TTG CCC TCT TTC CTT CTT TTG GAG	175
Leu Pro Ser Phe Leu Leu Leu Glu	
25 30	

(2) INFORMATION FOR SEQ ID NO: 198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 49..285
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.7
 seq VIGSLLVLTMLTC/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

```

ACATCACAAA AATTAGGTGA CCATGGTTAT GATAATTCTT TGCCTAGT ATG CAT CCA      57
                                   Met His Pro

TTT CTA GCT GCC CAC GGA CCT GCA TTT CAC AAA GGC TAC AAG CAT AGC      105
Phe Leu Ala Ala His Gly Pro Ala Phe His Lys Gly Tyr Lys His Ser
-75                               -70                               -65

ACA ATT AAC ATT GTG GAT ATT TAT CCA ATG ATG TGC CAC ATC CTG GGA      153
Thr Ile Asn Ile Val Asp Ile Tyr Pro Met Met Cys His Ile Leu Gly
-60                               -55                               -50                               -45

TTA AAA CCA CAT CCC AAT AAT GGG ACC TTT GGT CAT ACT AAG TGC TTG      201
Leu Lys Pro His Pro Asn Asn Gly Thr Phe Gly His Thr Lys Cys Leu
                               -40                               -35                               -30

TTA GTT GAC CAG TGG TGC ATT AAT CTC CCA GAA GCC ATC GCG ATT GTT      249
Leu Val Asp Gln Trp Cys Ile Asn Leu Pro Glu Ala Ile Ala Ile Val
-25                               -20                               -15

ATC GGT TCA CTC TTG GTG TTA ACC ATG CTA ACA TGC CGC CGG              291
Ile Gly Ser Leu Leu Val Leu Thr Met Leu Thr Cys Arg Arg
-10                               -5                               1

```

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 33..74
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.7
 seq IWPMASVATLWS/FT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

```

ATCTTAGTGT GACACATGAA CCCCTCCCCT TC ATG ATC TGG CCT ATG TCT GCC      53
                                   Met Ile Trp Pro Met Ser Ala
                                   -10

```

TCT GTA GCT ACT CTC TGG TCC TTT ACC TCT TAC ATA AGC TAC CCA AGC 101
Ser Val Ala Thr Leu Trp Ser Phe Thr Ser Tyr Ile Ser Tyr Pro Ser
-5 1 5

AGG TTT TAC TAT GAT GCT TGG
Arg Phe Tyr Tyr Asp Ala Trp
10 15

(2) INFORMATION FOR SEQ ID NO: 200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 12..104
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq LFIYLVFVECLLC/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

AAGGGTAATG G ATG GGA ATT GAT ATT TTC TAT CCT TCA CAC ATC CCA GAC 50
Met Gly Ile Asp Ile Phe Tyr Pro Ser His Ile Pro Asp
-30 -25 -20

TTT CAT CCT ATT CAT TTA TTC ATT TAT CTA GTG TTT GTA GAG TGC CTT 98
Phe His Pro Ile His Leu Phe Ile Tyr Leu Val Phe Val Glu Cys Leu
-15 -10 -5

CTG TGT ACC AGG AAC TGR GAW AGK TTG TCC KGA TTC AAC TGT GAT AAC 146
Leu Cys Thr Arg Asn Xaa Xaa Xaa Leu Ser Xaa Phe Asn Cys Asp Asn
1 5 10

GCT CAA ATA ATC TTC ACA ACA GGC TCA TCC TCT AGT GGA GGA AAT AAA 194
Ala Gln Ile Ile Phe Thr Thr Gly Ser Ser Ser Ser Gly Gly Asn Lys
15 20 25 30

CCA TTT AAA AGT AGT TTA TGT ACA GTA CAT AGA GGC CAA GAA AGG GAA 242
Pro Phe Lys Ser Ser Leu Cys Thr Val His Arg Gly Gln Glu Arg Glu
35 40 45

AGA ATA GAG TGC CAA GGG AAT GGG
Arg Ile Glu Cys Gln Gly Asn Gly
50

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 24..284
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq LILQASLKGELEA/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

```

AAATAGCTGA TTATGAACGT TTG ATG AAA GAA CTA AAT CAA AAG TTA ACT AAT      53
                        Met Lys Glu Leu Asn Gln Lys Leu Thr Asn
                        -85                                -80

AAA AAC AAC AAG ATA GAA GAT TTG GAG CAA GAA ATA AAA ATT CAA AAA      101
Lys Asn Asn Lys Lys Ile Glu Asp Leu Glu Gln Glu Ile Lys Ile Gln Lys
      -75                                -70                                -65

CAG AAA CAA GAA ACC CTA CAA GAA GAA ATA ACT TCA TTA CAG TCT TCA      149
Gln Lys Gln Glu Thr Leu Gln Glu Glu Ile Thr Ser Leu Gln Ser Ser
      -60                                -55                                -50

GTA CAA GAA TAT GAA GAA AAA AAC WCC AAA ATC AAG CAA TTG CTT GTG      197
Val Gln Glu Tyr Glu Glu Lys Asn Xaa Lys Ile Lys Gln Leu Leu Val
      -45                                -40                                -35

AAA ACC AAA AAG GAA CTG GCA GAT TCA AAG CAA GCA GAA ACT GAT CAC      245
Lys Thr Lys Lys Glu Leu Ala Asp Ser Lys Gln Ala Glu Thr Asp His
      -25                                -20                                -15

TTA ATA CTT CAA GCA TCT TTA AAA GGT GAG CTG GAG GCA AGC CAG CAG      293
Leu Ile Leu Gln Ala Ser Leu Lys Gly Glu Leu Glu Ala Ser Gln Gln
      -10                                -5                                1

CAA GTA GAA GTC TAT AAA GTA AGG GTT TTA CTT TTT AAG ATT AAA AAA      341
Gln Val Glu Val Tyr Lys Val Arg Val Leu Leu Phe Lys Ile Lys Lys
      5                                10                                15

ATG TTT TTT CAT GTA GAA GTG AGG AAC GGG      371
Met Phe Phe His Val Glu Val Arg Asn Gly
      20                                25

```

(2) INFORMATION FOR SEQ ID NO: 202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 33..371
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq RLLLCILIIVCYI/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

```

ACAGTCCTAC CTTTGCTGAT GCCTACTCTA AT ATG GGA AAC ACT CTA AAG GAG      53
                               Met Gly Asn Thr Leu Lys Glu
                               -110

ATG CAG GAT GTT CAG GGA GCC TTG CAG TGT TAT ACG CGT GCC ATC CAA      101
Met Gln Asp Val Gln Gly Ala Leu Gln Cys Tyr Thr Arg Ala Ile Gln
-105                      -100                      -95

ATT AAT CCT GCA TTT GCA GAT GCA CAT AGC AAT CTG GCT TCC ATT CAT      149
Ile Asn Pro Ala Phe Ala Asp Ala His Ser Asn Leu Ala Ser Ile His
-90                      -85                      -80                      -75

AAG GAT TCA GGG AAT ATT CCA GAA GCC ATA GCT TCT TAC CGC ACG GCT      197
Lys Asp Ser Gly Asn Ile Pro Glu Ala Ile Ala Ser Tyr Arg Thr Ala
                      -70                      -65                      -60

CTG AAA CTT AAG CCT GAT TTT CCT GAT GCT TAT TGT AAC TTG GCT CAT      245
Leu Lys Leu Lys Pro Asp Phe Pro Asp Ala Tyr Cys Asn Leu Ala His
                      -55                      -50                      -45

TGC CTG CAG ATT GTC TGT GAT TGG ACA GAC TAT GAT GAG CGA ATG AAG      293
Cys Leu Gln Ile Val Cys Asp Trp Thr Asp Tyr Asp Glu Arg Met Lys
-40                      -35                      -30

AAG TTG GTC AGT ATT GTG GCT GAC CAG TTA GAG AAG AAT AGG TTG CTT      341
Lys Leu Val Ser Ile Val Ala Asp Gln Leu Glu Lys Asn Arg Leu Leu
-25                      -20                      -15

CTG TGC ATC CTC ATC ATA GTA TGC TAT ATC CTC TTT CTC ATG      383
Leu Cys Ile Leu Ile Ile Val Cys Tyr Ile Leu Phe Leu Met
-10                      -5                      1

```

(2) INFORMATION FOR SEQ ID NO: 203:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 92..208
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq VAYAIPSIPSLFC/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

```
ACATGTTGAG TACTTTTTCC TCACCTGTTT TTCCATTCCT GTTAGCCGGA GCAAAGGGC   60
CTCCAAC TCC TCTTTTAGAG AGAAATGACT A ATG CTC ATA CTA GCA GAT ACC   112
                               Met Leu Ile Leu Ala Asp Thr
                               -35

AGA CGT GTC CAA GGA GGT ACC TTG GGC TTA ATT CCA GCA GTT CTC AAC   160
Arg Arg Val Gln Gly Gly Thr Leu Gly Leu Ile Pro Ala Val Leu Asn
   -30               -25               -20

AGA GTC CAC GTG GCA TAT GCT ATA CCC AGC ATA CCT AGC CTC TTC TGC   208
Arg Val His Val Ala Tyr Ala Ile Pro Ser Ile Pro Ser Leu Phe Cys
   -15               -10               -5

CAG CGC TGG   217
Gln Arg Trp
1
```

(2) INFORMATION FOR SEQ ID NO: 204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 343..402
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6

seq CVFLFPLISNTSS/YK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

```

CACACAATTA ATATTAATGG ATAACTAATT GGAGTAATGA TTATTAGCTA CTGAATGCTG      60
ATAATAGAAG TCATATTTAA ATGCTTACTT AGTTACTTAA GTTAGTCAAG GACTCTGAAA     120
AAAATAAGGT TTAAAGTTAA CAGTGTCAATC AGTCATTCCC AGTTATCTTC TTATTTAAGA     180
ACAAGATGGT AATGCAGTTG CCTTTGTTTA TTAAATAGA AAAAAATTAAA TCAGGATAAA     240
ATGACCCAAC TACAGTGATG TATTTGGACA CACTACTTCT TATCTTTCAA TATAGACTTT     300
TATTTCTGGA TTACCATAGA TGGAAATAGT ATTACTGGAC AT ATG TTG GTA GGT      354
                               Met Leu Val Gly
                               -20

ATT TAC TTC TGT GTT TTT CTT TTT CCC TTA ATT TCG AAT ACT TCT AGC      402
Ile Tyr Phe Cys Val Phe Leu Phe Pro Leu Ile Ser Asn Thr Ser Ser
   -15                               -10                               -5

TAC AAA AAT TGT CAT AAA ACT TTG CAA CAC ACT ATA CCT CCC CAC GGG      450
Tyr Lys Asn Cys His Lys Thr Leu Gln His Thr Ile Pro Pro His Gly
   1                               5                               10                               15

```

(2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..126
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq LLLQGACPLIFL/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

```

ATG TTT CTC GCT CCC TCT CTG CTG ATC ACA AAG CTG CTG ACC GGG TCA      48
Met Phe Leu Ala Pro Ser Leu Leu Ile Thr Lys Leu Leu Thr Gly Ser
   -40                               -35                               -30

GAA AGT CCT GAT GGA AAT CCA CCA GCG CTG GGC AGG CCC CTC CTC CTC      96
Glu Ser Pro Asp Gly Asn Pro Pro Ala Leu Gly Arg Pro Leu Leu Leu
   -25                               -20                               -15

```

```

CAG GGA GCT TGT CCT TGC CTA ATT TTT CTT CGT CCT GAT GAG AAC AAA    144
Gln Gly Ala Cys Pro Cys Leu Ile Phe Leu Arg Pro Asp Glu Asn Lys
-10                      -5                      1                      5

AAA GAG GGG GRG GAG GAA AAG AAA AAC CAC AAA CTT CCT TTG AAA ACC    192
Lys Glu Gly Xaa Glu Glu Lys Lys Asn His Lys Leu Pro Leu Lys Thr
          10                      15                      20

AGC TTA GGG                                201
Ser Leu Gly
          25

```

(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 235..288
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq SKSCLFYLQKVSG/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

```

AAAGGTGGCT TCAGGACCAC CTCCTGAGAG CTTGTTGTA TTTCATGTAT ATTTCCCCAA    60
ATATATCAGC ATCTGACCCT TGGCTTCTGG GAGAAAGACA GAGGCGGAAC CCTGGCCGCC    120
CCAGAGAGAG GCAGCTGTGG GGGCAGAGAT GTAACAACCC TTTGAACCTT GACCTTGGAC    180
GCCAGGCTGT CCGGGAGCTT CTCCCACAAT GGCTGTTTTG GGGATGTGAC CTGG ATG    237
                                   Met
GAC CCA TCT GCT AGC AAA TCC TGT CTG TTT TAC CTC CAA AAA GTA TCT    285
Asp Pro Ser Ala Ser Lys Ser Cys Leu Phe Tyr Leu Gln Lys Val Ser
      -15                      -10                      -5

GGA ATT CCA GGG CTT CTC ACC                                306
Gly Ile Pro Gly Leu Leu Thr
      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 54..191
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.5
 seq RWLCLQAYLASFS/LE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

ACGTGTCCTC AGGATTTTCC TCTTGGGCTG GACAGTTTGC TCCCCTGGAG GGT ATG	56
Met	
AGC CTG ACT GCT AGT GGG CCA AGA GCT GCC TGG GAG GAA AGG GTG GGG	104
Ser Leu Thr Ala Ser Gly Pro Arg Ala Ala Trp Glu Glu Arg Val Gly	
-45 -40 -35 -30	
GGT CTC CAC ACT TGG GGT GCC AAC ATT CCT ACC GCC CCT GAT TCC CAG	152
Gly Leu His Thr Trp Gly Ala Asn Ile Pro Thr Ala Pro Asp Ser Gln	
-25 -20 -15	
CGG TGG CTC TGT CTT CAG GCG TAC CTG GCA TCC TTC AGT CTT GAG AGC	200
Arg Trp Leu Cys Leu Gln Ala Tyr Leu Ala Ser Phe Ser Leu Glu Ser	
-10 -5 1	
CCC CAC AGA ATC TAC CTK GAA TCT CCT CCC ACG CTC CTT TTC CCC CCG	248
Pro His Arg Ile Tyr Leu Glu Ser Pro Pro Thr Leu Leu Phe Pro Pro	
5 10 15	
CCG	251
Pro	
20	

(2) INFORMATION FOR SEQ ID NO: 208:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 242 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 117..182
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq AQLASPLLPGATP/VA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

```
ACCGCAGAAA ATGCTAGGTG CAAAGTTTGT CGAAAGAAAG GTGAGGATGA CAAATTGATC    60
TTGTGTGATG AGTGTAAATA AGCCTTYCCA CCTGTTTTGT CTGAGGCCGG CCCTCT ATG    119
                                     Met
AAG TAC CAG ATG GTG AGT GGC AGT GCC CAG CTT GCC AGC CCG CTA CTG    167
Lys Tyr Gln Met Val Ser Gly Ser Ala Gln Leu Ala Ser Pro Leu Leu
-20                               -15                               -10
CCA GGC GCA ACT CCC GTG GCA GGA ACT ATA CTG AAG AGT CTG CTT CTG    215
Pro Gly Ala Thr Pro Val Ala Gly Thr Ile Leu Lys Ser Leu Leu Leu
-5                               1                               5                               10
AGG ACA GTG AAG ATG ATG AGA GTG ATG                                242
Arg Thr Val Lys Met Met Arg Val Met
15                               20
```

(2) INFORMATION FOR SEQ ID NO: 209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 229..333
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq CFWGLMYXWLLLG/SX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

```
ACATCTGATC GATAATTATG TCACCTGTAC CTGTCGCCAG CTTGTCTTGT TATGACGTTA    60
GTTTTACTGC TAGAAATATC TAGTAGATGG CTGGAAATCT GCAGGCAAAG TGCAGAGGGA    120
GTGAGCCTGC GAGGAGAGGG SCTGGGCAAA GTGAMBGCCC TGGGCCGCAG AGTTCTTATC    180
```

TAAAAAATGG GAACAGTAGT GTCTTCCTAA AGGCACCATG GACTTAAA ATG AAT GGC	237
	Met Asn Gly
	-35
ACG TTT CCT GGG ACT TAT GTA TAT TTG GTT GCT TAT GGG GAC TTA CGT	285
Thr Phe Pro Gly Thr Tyr Val Tyr Leu Val Ala Tyr Gly Asp Leu Arg	
-30 -25 -20	
ATA TTT GGT TGC TTT TGG GGA CTT ATG TAT ATK TGG TTG CTT TTG GGG	333
Ile Phe Gly Cys Phe Trp Gly Leu Met Tyr Xaa Trp Leu Leu Leu Gly	
-15 -10 -5	
TCT NAA GGG	
Ser Xaa Gly	342
1	

(2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 131..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 66..157
id AA134726
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 216..282
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 152..218
id AA134726
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 283..342
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 220..279
id AA134726
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 64..103
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..40
 id AA134726
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 98..130
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 34..66
 id AA134726
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 81..285
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 1..205
 id R17226
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 50..112
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 12.7
 seq ILFLLSWSGPLQG/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

GAGGCTGACT GTACGTTTCCT TCTACTCTGG CACCACTCTC CAGGCTGCC ATG GGG CCC	58
Met Gly Pro	
-20	
AGC ACC CCT CTC CTC ATC TTG TTC CTT TTG TCA TGG TCG GGA CCC CTC	106
Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp Ser Gly Pro Leu	
-15 -10 -5	
CAA GGA CAG CAG CAC CAC CTT GTG GAG TAC ATG GAA CGC CGA CTA GCT	154
Gln Gly Gln Gln His His Leu Val Glu Tyr Met Glu Arg Arg Leu Ala	
1 5 10	
GCT TTA GAG GAA CGG CTG GCC CAG TGC CAG GAC CAG AGT AGT CGG CAT	202
Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln Asp Gln Ser Ser Arg His	
15 20 25 30	
GCT GCT GAG CTG CGG AAC TTC AAG AAC AAG ATG CTG CCA CTG CTG GAG	250
Ala Ala Glu Leu Arg Asn Phe Lys Asn Lys Met Leu Pro Leu Leu Glu	
35 40 45	
GTG GCA GAG AAG GAG CGG GAG GCA CTC AGA ACT GAG GCC GRC ACC ATC	293
Val Ala Glu Lys Glu Arg Glu Ala Leu Arg Thr Glu Ala Xaa Thr Ile	
50 55 60	
TCN NVN GGA GTG GAT CGT CTG GAG CGG GAG GTA GAC TAT CTG	340
Ser Xaa Gly Val Asp Arg Leu Glu Arg Glu Val Asp Tyr Leu	

(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
(B) LOCATION: 124..310
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 46..232
id T39765
est

(ix) FEATURE:

- [illegible]

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 76..141
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10.5
seq LMLLVSSSLSPVQG/VL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

AAAATAGGAG	TCTCTGGTAC	TGCAAACCCA	CAGCCTGGAC	TCAGAGCTCA	AGTCTGAACT	60
CTACCTCCAG	ACAGA	ATG AAG TTC ATC	TCG ACA TCT CTG	CTT CTC ATG CTG	111	
		Met Lys Phe Ile Ser Thr Ser	Leu Leu Leu Met Leu			
		-20	-15			
CTG GTC AGC AGC CTC TCT CCA GTC CAA GGT GTT CTG GAG GTC TAT TAC	159					
Leu Val Ser Ser Leu Ser Pro Val Gln Gly Val Leu Glu Val Tyr Tyr						
-10 -5 1 5						
ACA AGC TTG AGG TGT AGA TGT GTC CAA GAG AGC TCA GTC TTT ATC CCT	207					
Thr Ser Leu Arg Cys Arg Cys Val Gln Glu Ser Ser Val Phe Ile Pro						
10 15 20						

```

AGA CGC TTC ATT GAT CGA ATT CAA ATC TTG CCC CGT GGG AAT GGT TGT      255
Arg Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn Gly Cys
      25                      30                      35

CCA AGA AAA GAA ATC ATA GTC TGG AAG AAG AAC AAG TCA ATT GTG TGT      303
Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile Val Cys
      40                      45                      50

GTG GAC CTC AAG CAT AGG                                          321
Val Asp Leu Lys His Arg
      55                      60

```

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 241..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..186
id T07474
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 16..156
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8
seq VLELLAAVCLVRG/GH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

```

AGTTTACGTG CCATC ATG AAT TAT CAG TAT GGT TTC AAC ATG GTC ATG TCT      51
      Met Asn Tyr Gln Tyr Gly Phe Asn Met Val Met Ser
            -45                      -40

CAT CCA CAC GCT GTC AAT GAG ATT GCA CTA AGC CTG AAC AAC AAG AAT      99
His Pro His Ala Val Asn Glu Ile Ala Leu Ser Leu Asn Asn Lys Asn
-35                      -30                      -25                      -20

CCC AGA ACA AAA GCC CTT GTC TTA GAA CTG TTG GCA GCC GTT TGT CTT      147
Pro Arg Thr Lys Ala Leu Val Leu Glu Leu Leu Ala Ala Val Cys Leu
      -15                      -10                      -5

GTC AGA GGC GGG CAT GAA ATC ATT TTA TCA GCA TTT GAT AAC TTT AAA      195

```

Val	Arg	Gly	Gly	His	Glu	Ile	Ile	Leu	Ser	Ala	Phe	Asp	Asn	Phe	Lys	
		1					5					10				
GAG	GTT	TGT	GGA	GAA	AAA	CAG	CGC	TTT	GAG	AAG	TTG	ATG	GAA	CAT	TTC	243
Glu	Val	Cys	Gly	Glu	Lys	Gln	Arg	Phe	Glu	Lys	Leu	Met	Glu	His	Phe	
	15					20					25					
AGG	AAT	GAA	GAC	AAT	AAC	ATA	GAT	TTT	ATG	GTG	GCT	TCT	ATG	CAG	TTT	291
Arg	Asn	Glu	Asp	Asn	Asn	Ile	Asp	Phe	Met	Val	Ala	Ser	Met	Gln	Phe	
	30				35					40					45	
ATT	AAT	ATT	GTA	GTC	CAT	TCA	GTA	GAA	GAT	ATG	AAT	TTC	AGA	GTT	CAC	339
Ile	Asn	Ile	Val	Val	His	Ser	Val	Glu	Asp	Met	Asn	Phe	Arg	Val	His	
				50					55					60		
CTG	CAG	TAT	GAA	TTT	ACC	AAA	TTA	GGC	CTG	GMC	GAA	TAC	TTG	GRC	AAG	387
Leu	Gln	Tyr	Glu	Phe	Thr	Lys	Leu	Gly	Leu	Xaa	Glu	Tyr	Leu	Xaa	Lys	
			65					70					75			
CTG	AAA	CAC	ACT	GAG	AGT	GAC	AAG	CTT	CAA	GTC	CAG	ATC				426
Leu	Lys	His	Thr	Glu	Ser	Asp	Lys	Leu	Gln	Val	Gln	Ile				
		80					85					90				

(2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 246..387
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..142
id HUM75821
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 246..387
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..142
id T08488
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 261..387

(C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..127
 id R54273
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 205..288
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.7
 seq LVMCFLSYFGTFA/VE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

```

ATTGTAATT TTCAGCTCAC AAATGATGAA GAAATCCATA ACGTCGGAAC TTCCTTGACC      60
TTTGGATTTG GCACATTGAC CTGCTGGATC CAGGCTGCGC TGACACTCAA GGTCAACATC      120
AASAATGAAG GACGGAGAGT TGAATTCCA CGGGTTATTC TGTCGGCATC TATCACTCTC      180
TGTGTGGTCC TCTACTTCAT CCTC ATG GCC CAA AGC ATC CAC ATG TAT GCA          231
                Met Ala Gln Ser Ile His Met Tyr Ala
                -25                               -20

GCC AGG GTC CAG TGG GGC CTG GTC ATG TGC TTC CTG TCT TAT TTT GGC          279
Ala Arg Val Gln Trp Gly Leu Val Met Cys Phe Leu Ser Tyr Phe Gly
                -15                               -10                               -5

ACC TTT GCC GTG GAG TTC CGG CAT TAC CGC TAT GAG ATT GTT TGC TCT          327
Thr Phe Ala Val Glu Phe Arg His Tyr Arg Tyr Glu Ile Val Cys Ser
                1                               5                               10

GAG TAC CAG GAG AAT TTC CTA AGC TTC TCA GAA AGC CTG TCA GAA GCT          375
Glu Tyr Gln Glu Asn Phe Leu Ser Phe Ser Glu Ser Leu Ser Glu Ala
                15                               20                               25

TCT GAA TAT CAG                                                                387
Ser Glu Tyr Gln
30

```

(2) INFORMATION FOR SEQ ID NO: 214:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 124..335
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..212
id AA081335
est

(ix) FEATURE:

[illegible]

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 296..335
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 82..121
id H88204
est

(ix) FEATURE:

[illegible]

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 76..138
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.1
seq LHLFHLIRPXQG/WX

(xi) SEQUENCE DESCRIPTION: SEO ID NO: 214:

ACTCTCTGCT	GA	ACTCCCAA	AGGGAGTGTG	TGTATTTCTT	CCC	GTTCTTN	ATCAGAGCCC	60								
CCAAAATAAG	TAGGA	ATG	GGC	AGT	GGC	TAT	TCA	CAT	TCA	CTA	CAC	CTT	TTC	111		
		Met	Gly	Ser	Gly	Tyr	Ser	His	Ser	Leu	His	Leu	Phe			
			-20					-15					-10			
CAT	TTG	CTA	ATA	AGG	CCC	TGS	CAA	GGT	TGG	RAG	GRA	ATT	GTC	CCT	GCC	159
His	Leu	Leu	Ile	Arg	Pro	Xaa	Gln	Gly	Trp	Xaa	Xaa	Ile	Val	Pro	Ala	
			-5						1				5			
TGC	TTC	TGG	AGA	AAG	AAG	ATA	TTG	ACA	CCA	TCT	ACG	GGC	ACC	ATG	GAA	207
Cys	Phe	Trp	Arg	Lys	Lys	Ile	Leu	Thr	Pro	Ser	Thr	Gly	Thr	Met	Glu	
		10					-15					20				
CTG	CTT	CAA	GTG	ACC	ATT	CTT	TTT	CTT	CTG	CCC	AGT	ATT	TGC	AGC	AGT	255
Leu	Leu	Gln	Val	Thr	Ile	Leu	Phe	Leu	Leu	Pro	Ser	Ile	Cys	Ser	Ser	
	25					30					35					

AAC AGC ACA GGT GTT TTA GAG GCA GCT AAT AAT TCA CTT GTT GTT ACT 303
Asn Ser Thr Gly Val Leu Glu Ala Ala Asn Asn Ser Leu Val Val Thr
40 45 50 55

ACA ACA AAA CCA TCT ATA ACA ACA CCA AAC ACG TGG 339
Thr Thr Lys Pro Ser Ile Thr Thr Pro Asn Thr Trp
60 65

(2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 209..324
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..116
id AA081350
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 277..324
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 3..50
id AA046671
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 157..204
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq CFSLVLLLSIWT/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

AGGGAAATCC GGATGTCTCG GTTATGAAGT GGAGCAGTGA GTGTGAGCCT CAACATAGTT 60

CCAGAACTCT CCATCCGGAC TAGTTATTGA GCATCTGCCT CTCATATCAC CAGTGGCCAT 120

CTGAGGTGTT TCCCTGGCTC TGAAGGGGTA GGCACG ATG GCC AGG TGC TTC AGC 174
Met Ala Arg Cys Phe Ser
-15

CTG	GTG	TTG	CTT	CTC	ACT	TCC	ATC	TGG	ACC	ACG	AGG	CTC	CTG	GTC	CAA	222
Leu	Val	Leu	Leu	Leu	Thr	Ser	Ile	Trp	Thr	Thr	Arg	Leu	Leu	Val	Gln	
-10					-5					1				5		
GGC	TCT	TTG	CGT	GCA	GAA	GAG	CTT	TCC	ATC	CAG	GTG	TCA	TGC	AGA	ATT	270
Gly	Ser	Leu	Arg	Ala	Glu	Glu	Leu	Ser	Ile	Gln	Val	Ser	Cys	Arg	Ile	
			10					15					20			
ATG	GNN	RTC	ACC	CTT	GTG	AGC	AAA	AAG	GCG	AAC	CAG	CAG	CTG	AAT	TTC	318
Met	Xaa	Xaa	Thr	Leu	Val	Ser	Lys	Lys	Ala	Asn	Gln	Gln	Leu	Asn	Phe	
		25					30					35				
ACA	GAA	NNV	NAA	GGA	GGC	CWW	WAR	GCT	GCT	GGG	ACT	AAG	TTT	GGC		363
Thr	Glu	Xaa	Xaa	Gly	Gly	Xaa	Xaa	Ala	Ala	Gly	Thr	Lys	Phe	Gly		
	40					45					50					

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 20..194
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 144..318
id AA045920
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 194..257
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 319..382
id AA045920
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 20..226
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 153..359
id N25870
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 220..262
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 355..397
 id N25870
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 20..176
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 143..299
 id H99323
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 212..267
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 92
 region 335..390
 id H99323
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 67..262
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 1..196
 id AA150024
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 171..269
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.7
 seq MTCLSVLFGYATS/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

AATCTTGTC	GAAGTCGTCG	AAAATATTTA	CACCAGCAGC	TCCAGTTCAT	ACCAATAAAG	60
AAGATCCTGC	TACCCAAACT	AATTTGGGRW	TTATCCAWGC	ATTTGKCGCT	GCCATATCAG	120
TTATTAWTGK	ATCYGAATTG	GGTGATAAGA	CATTTTTTAT	AGCAGCCATC	ATG GCA	176
					Met Ala	
ATG CGC TAT AAC CGC CTG ACC GTG CTG GCT GGT GCA ATG CTT GCC TTG						224
Met Arg Tyr Asn Arg Leu Thr Val Leu Ala Gly Ala Met Leu Ala Leu						
-30		-25		-20		
GGA CTA ATG ACA TGC TTG TCA GTT TTG TTT GGC TAT GCC ACC AGT CAT						272
Gly Leu Met Thr Cys Leu Ser Val Leu Phe Gly Tyr Ala Thr Ser His						
-15		-10		-5		1
CCC CAG GGC CTA TAC ATA						290
Pro Gln Gly Leu Tyr Ile						

(2) INFORMATION FOR SEQ ID NO: 217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- [illegible]

(ix) FEATURE:

- (A) NAME/KEY: other
(B) LOCATION: 288..318
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..31
id R51759
est

(ix) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: 211..288
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.3
 seq RQLLLPLPPFSFP/AP
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

|                                                                 |            |            |                                 |            |            |     |
|-----------------------------------------------------------------|------------|------------|---------------------------------|------------|------------|-----|
| AGTCAATTCT                                                      | AGGAGCCATC | AAGCATGAAA | GTGGTTCTGT                      | CTCCTGAGCG | CAASCTCGCC | 60  |
| GGACCCCTGG                                                      | GCGAAGGCCT | GGACTTGCAG | ATGTGTGTTC                      | CCTGTGCGGG | TGGACAGAGG | 120 |
| GGGCCCTTAT                                                      | GACCCACATT | GCAGCCCCAT | TCCACCACCC                      | CTTCCTCCCC | AGAGCAGTCT | 180 |
| CTGCCGAGGG                                                      | ACAGCACCTG | TGTCCCTTCG | ATG CCA CAA CAG CCA GTT GAA CAG |            |            | 234 |
|                                                                 |            |            | Met Pro Gln Gln Pro Val Glu Gln |            |            |     |
|                                                                 |            |            | -25                             |            | -20        |     |
| GGG AGC CCT TTG CTC AGG CAG CTT CTC CTG CCT CTC CCT CCT TTC TCC |            |            |                                 |            |            | 282 |
| Gly Ser Pro Leu Leu Arg Gln Leu Leu Leu Pro Leu Pro Pro Phe Ser |            |            |                                 |            |            |     |
|                                                                 | -15        |            | -10                             |            | -5         |     |

TTC CCT GCC CCA TCC CCG TGC CCT TCT TGG CCT GTG GCG CTG GGG AGC 330  
 Phe Pro Ala Pro Ser Pro Cys Pro Ser Trp Pro Val Ala Leu Gly Ser  
                   1                                  5                                  10

CAT GGT GTG GCA TAC TGG GGC TCC TGC TCC TTG GGS CAC 369  
 His Gly Val Ala Tyr Trp Gly Ser Cys Ser Leu Gly His  
           15                                  20                                  25

(2) INFORMATION FOR SEQ ID NO: 218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 117..390
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..274  
id C16636  
est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 121..360
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2  
seq RASLLPMLLGSWA/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

AAAAAAGAGC TGGTTCCTTG GCAGGCTGGA GGGCAGGAGC TGGGGCCACG CTGGTCTGGG 60

ATAGTTGGGC AGGGAGGCTG TCTACCTGGT CTTCCAGAAT GGACGGCCCT GTGGCAGAGC 120

ATG CCA AGC AGG AGC CCT TTC ACG TGG TCA CAC CTC TGT TGG AGA GCT 168  
 Met Pro Ser Arg Ser Pro Phe Thr Trp Ser His Leu Cys Trp Arg Ala  
 -80 -75 -70 -65

GGG CGC TGT CCC AGG TGG CGG GCA TGC CTG TCT TCC TCA AGT GTG AGA 216  
 Gly Arg Cys Pro Arg Trp Arg Ala Cys Leu Ser Ser Ser Val Arg  
                   -60                                  -55                                  -50

ATG TGC AGC CCA GCG GCT CCT TCA AGA TTC GGG GCA TTG GGC ATN TCT 264  
 Met Cys Ser Pro Ala Ala Pro Ser Arg Phe Gly Ala Leu Gly Xaa Ser  
                   -45                                  -40                                  -35

GCC AGG AGA TGG CCA AGA AGG GAT GCA GAC ACC TGG TGT GCT CCT CAG 312

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Arg | Arg | Trp | Pro | Arg | Arg | Asp | Ala | Asp | Thr | Trp | Cys | Ala | Pro | Gln |     |
|     |     | -30 |     |     |     |     | -25 |     |     |     |     | -20 |     |     |     |     |
| GGG | GTA | ATG | CGG | GCA | TCG | CTG | CTG | CCT | ATG | CTG | CTA | GGA | AGC | TGG | GCA | 360 |
| Gly | Val | Met | Arg | Ala | Ser | Leu | Leu | Pro | Met | Leu | Leu | Gly | Ser | Trp | Ala |     |
|     | -15 |     |     |     |     | -10 |     |     |     |     | -5  |     |     |     |     |     |
| TTC | CTG | CCA | CCA | TCG | TGC | TCC | CCG | AGA | GCA |     |     |     |     |     |     | 390 |
| Phe | Leu | Pro | Pro | Ser | Cys | Ser | Pro | Arg | Ala |     |     |     |     |     |     |     |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

- [illegible]

(ix) FEATURE:

- (A) NAME/KEY: other  
 (B) LOCATION: 132..450  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 91  
                                 region 156..474  
                                 id AA142584  
                                 est

(ix) FEATURE:

- [illegible]

(ix) FEATURE:

- (A) NAME/KEY: other  
(B) LOCATION: 101..304  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 72..275  
id T18932

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 132..243
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 146..257  
id AA123074  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 165..284
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6  
seq LTYGIILTHGASG/DM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

```

AACGCTGTGG CGGGGCAGGC GAGGCGGTCTG CTTGAGCGC GCTAGTCAGC TCCCTGAAGG 60
GAGTGACGGC GGTGGGTGC CCGCGGCCAC TTTGCCTTC CCGGGGAGAT GTCCTTTGCT 120
TCTCAGATGT AAKGCACTT TAAGTTTGKW ATTCAACAGT GAAA ATG AGT CAT ACA 176
 Met Ser His Thr
 -40

GAG GTT AAA TTA AAA ATA CCT TTT GGA AAT AAA TTA CTA GAT GCT GTT 224
Glu Val Lys Leu Lys Ile Pro Phe Gly Asn Lys Leu Leu Asp Ala Val
-35 -30 -25

TGT TTG GTA CCT AAC AAG AGC TTA ACA TAT GGA ATA ATT CTT ACA CAT 272
Cys Leu Val Pro Asn Lys Ser Leu Thr Tyr Gly Ile Ile Leu Thr His
-20 -15 -10 -5

GGA GCA TCA GGA GAT ATG AAT CTT CCT CAT TTG ATG TCA CTG GCA TCC 320
Gly Ala Ser Gly Asp Met Asn Leu Pro His Leu Met Ser Leu Ala Ser
 1 5 10

CAT CTT GCA TCT CAT GGG TTT TTC TGC CTG AGA TTT ACC TGT AAA GGC 368
His Leu Ala Ser His Gly Phe Phe Cys Leu Arg Phe Thr Cys Lys Gly
 15 20 25

CTT AAT ATT GTA CAT AGA ATT AAG GCG TAT AAA TCA GTT TTG AAT TAC 416
Leu Asn Ile Val His Arg Ile Lys Ala Tyr Lys Ser Val Leu Asn Tyr
 30 35 40

CTG AAG ACA TCA GGM RAA TAC AAA CTT GCA GGT 449
Leu Lys Thr Ser Gly Xaa Tyr Lys Leu Ala Gly
45 50 55

```

## (2) INFORMATION FOR SEQ ID NO: 220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 75..254
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..180  
id T31666  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 73..126
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 88..141  
id R58665  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 23..77
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 39..93  
id R58665  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 157..231
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 63..137  
id R14990  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 95..144
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 1..50  
id R14990  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 135..254
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..120  
id T26956



est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 31..150
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6  
seq LCXEFXSVASCD/AV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

```

AAAAAGGGGC GGTGCAGAGG CGGCAGGAAG ATG GAG TTG GGG AGT TGC CTG GAG 54
 Met Glu Leu Gly Ser Cys Leu Glu
 -40 -35

GGC GGG AGG GAG GCG GCG GAG GAA GAG GGC GAG CCT GAG GTG AAA AAG 102
Gly Gly Arg Glu Ala Ala Glu Glu Glu Gly Glu Pro Glu Val Lys Lys
-30 -25 -20

CGG CGA CTT CTG TGT STR GAG TTT RCC TCG GTC GCA AGC TGC GAT GCC 150
Arg Arg Leu Leu Cys Xaa Glu Phe Xaa Ser Val Ala Ser Cys Asp Ala
-15 -10 -5

GCA GTG GCT CAG TGC TTC CTG GCC GAK AAC GAC TGG GAG ATG GAA AGG 198
Ala Val Ala Gln Cys Phe Leu Ala Xaa Asn Asp Trp Glu Met Glu Arg
 1 5 10 15

GCT CTG AAC TCC TAC TTC GAG CCT CCG GTG GAG GAG AGC GCC TTG GAA 246
Ala Leu Asn Ser Tyr Phe Glu Pro Pro Val Glu Glu Ser Ala Leu Glu
 20 25 30

CGC CGA CCA DGG 258
Arg Arg Pro Xaa
 35

```

## (2) INFORMATION FOR SEQ ID NO: 221:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 138..317
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 52..231  
id AA099777  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 85..135  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
                           region 1..51  
                           id AA099777  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 138..222  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 83..167  
                           id HSB16C031  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 80..135  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
                           region 27..82  
                           id HSB16C031  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 145..314  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 91  
                           region 43..212  
                           id AA068028  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 148..255  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.8  
                           seq AFVSGLLIGQCSS/QK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

```

AGGCAGTGAA TTGAGACCGG AGGGAATCTG GCCCCTAGAG GCTGGTACTT GGGCCCGAAA 60
CCCCCATCTC CGGCGGAGAG ACCGTCCGAG GTAATTGTCT GCCACGAGTG CACATTCTGA 120
AAACAGGRGR WTTTAAGKTT CCTAAAA ATG GGA AGA ACC TAC ATT GTA GAA GAG 174
 Met Gly Arg Thr Tyr Ile Val Glu Glu
 -35 -30

ACT GTT GGC CAG TAT CTT TCA AAC ATA AAT CTC CAA GGA AAG GCT TTT 222
Thr Val Gly Gln Tyr Leu Ser Asn Ile Asn Leu Gln Gly Lys Ala Phe
 -25 -20 -15

GTC TCT GGC CTT TTA ATA GGA CAG TGT TCG TCA CAA AAG GAT TAT GTG 270
Val Ser Gly Leu Leu Ile Gly Gln Cys Ser Ser Gln Lys Asp Tyr Val

```

-10

-5

1

5

ATT CTT GCC ACT AGA ACG CCA CCC AAA GAG GAG CAA AGT GAG AAC TTG 318  
Ile Leu Ala Thr Arg Thr Pro Pro Lys Glu Glu Gln Ser Glu Asn Leu  
10 15 20

## (2) INFORMATION FOR SEQ ID NO: 222:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 227..433
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..207  
id R16604  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 432..474
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 207..249  
id R16604  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 227..440
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..214  
id N99558  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 109..171
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq CLSCLLIPLALWS/II

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

AGTATTTTAC ACTGAGATTG TCGGCTGCGG GTATATTCCA ATTCCCCGTC TCCTCATGAA 60

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TATGAAGTGA AGGGCTCTGA CCCTGGAAGT GGTCTAAGC AGGGCAAA ATG GGG TCT | 117 |
| Met Gly Ser                                                     |     |
| -20                                                             |     |
| CGG AAG TGT GGA GGC TGC CTA AGT TGT TTG CTG ATT CCG CTT GCA CTT | 165 |
| Arg Lys Cys Gly Gly Cys Leu Ser Cys Leu Leu Ile Pro Leu Ala Leu |     |
| -15 -10 -5                                                      |     |
| TGG AGT ATA ATC GTG AAC ATA TTA TTG TAT TTC CCG AAT GGG CAA ACT | 213 |
| Trp Ser Ile Ile Val Asn Ile Leu Leu Tyr Phe Pro Asn Gly Gln Thr |     |
| 1 5 10                                                          |     |
| TCC TAT GCA TCC AGC AAT AAA CTC ACC AAC TAC GTG TGG TAT TTT GAA | 261 |
| Ser Tyr Ala Ser Ser Asn Lys Leu Thr Asn Tyr Val Trp Tyr Phe Glu |     |
| 15 20 25 30                                                     |     |
| GGA ATC TGT TTC TCA GGC ATC ATG ATG CTT ATA GTA ACA ACA GTT CTT | 309 |
| Gly Ile Cys Phe Ser Gly Ile Met Met Leu Ile Val Thr Thr Val Leu |     |
| 35 40 45                                                        |     |
| CTG GTA CTG GAG AAT AAT AAC AAC TAT AAA TGT TGC CAG AGT GAA AAC | 357 |
| Leu Val Leu Glu Asn Asn Asn Asn Tyr Lys Cys Cys Gln Ser Glu Asn |     |
| 50 55 60                                                        |     |
| TGC AGC AAA AAA TAT GTG ACA CTG CTG TCA ATT ATC TTT TCT TCC CTC | 405 |
| Cys Ser Lys Lys Tyr Val Thr Leu Leu Ser Ile Ile Phe Ser Ser Leu |     |
| 65 70 75                                                        |     |
| GGA ATT GCT TTT TCT GGA TAC TGC CTG GTC ATC TCT GCC TTG GGT CTT | 453 |
| Gly Ile Ala Phe Ser Gly Tyr Cys Leu Val Ile Ser Ala Leu Gly Leu |     |
| 80 85 90                                                        |     |
| GTC CAA GGG CCA TAT TGC CGC                                     | 474 |
| Val Gln Gly Pro Tyr Cys Arg                                     |     |
| 95 100                                                          |     |

## (2) INFORMATION FOR SEQ ID NO: 223:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 128..341
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..214  
id N99558

est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 399..459  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
 region 278..338  
 id N99558  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 359..407  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
 region 237..285  
 id N99558  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 128..334  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 1..207  
 id R16604  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 333..386  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 207..260  
 id R16604  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 10..72  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.6  
 seq CLSCLLIPLALWS/II

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

|                                                                 |                                                         |    |
|-----------------------------------------------------------------|---------------------------------------------------------|----|
| AAGGGCAAA                                                       | ATG GGG TCT CGG AAG TGT GGA GGC TGC CTA AGT TGT TTG CTG | 51 |
|                                                                 | Met Gly Ser Arg Lys Cys Gly Gly Cys Leu Ser Cys Leu Leu |    |
|                                                                 | -20 -15 -10                                             |    |
| ATT CCG CTT GCA CTT TGG AGT ATA ATC GTG AAC ATA TTA TTG TAT TTC | 99                                                      |    |
| Ile Pro Leu Ala Leu Trp Ser Ile Ile Val Asn Ile Leu Leu Tyr Phe |                                                         |    |
| -5 1 5                                                          |                                                         |    |
| CCG AAT GGG CAA ACT TCC TAT GCA TCC AGC AAT AAA CTC ACC AAC TAC | 147                                                     |    |
| Pro Asn Gly Gln Thr Ser Tyr Ala Ser Ser Asn Lys Leu Thr Asn Tyr |                                                         |    |
| 10 15 20 25                                                     |                                                         |    |
| GTG TGG TAT TTT GAA GGA ATC TGT TTC TCA GGC ATC ATG ATG CTT ATA | 195                                                     |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Trp | Tyr | Phe | Glu | Gly | Ile | Cys | Phe | Ser | Gly | Ile | Met | Met | Leu | Ile |     |  |
|     |     |     |     | 30  |     |     |     |     | 35  |     |     |     |     | 40  |     |     |  |
| GTA | ACA | ACA | GTT | CTT | CTG | GTA | CTG | GAG | AAT | AAT | AAC | AAC | TAT | AAA | TGT | 243 |  |
| Val | Thr | Thr | Val | Leu | Leu | Val | Leu | Glu | Asn | Asn | Asn | Asn | Tyr | Lys | Cys |     |  |
|     |     |     | 45  |     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |  |
| TGC | CAG | AGT | GAA | AAC | TGC | AGC | AAA | AAA | TAT | GTG | ACA | CTG | CTG | TCA | ATT | 291 |  |
| Cys | Gln | Ser | Glu | Asn | Cys | Ser | Lys | Lys | Tyr | Val | Thr | Leu | Leu | Ser | Ile |     |  |
|     |     | 60  |     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     |  |
| ATC | TTT | TCT | TCC | CTC | GGA | ATT | GCT | TTT | TCT | GGA | TAC | TGC | CTG | GTC | ATC | 339 |  |
| Ile | Phe | Ser | Ser | Leu | Gly | Ile | Ala | Phe | Ser | Gly | Tyr | Cys | Leu | Val | Ile |     |  |
|     | 75  |     |     |     |     | 80  |     |     |     | 85  |     |     |     |     |     |     |  |
| TCT | GCC | TTG | GGT | CTT | GTC | CAA | GGG | CCA | TAT | TGC | CGC | ACC | CTT | GAT | GGC | 387 |  |
| Ser | Ala | Leu | Gly | Leu | Val | Gln | Gly | Pro | Tyr | Cys | Arg | Thr | Leu | Asp | Gly |     |  |
| 90  |     |     |     |     | 95  |     |     |     | 100 |     |     |     |     | 105 |     |     |  |
| TGG | GAG | TAT | GCT | TTT | GAA | GGC | ACT | RCT | GGA | CGT | TTC | CTT | ACA | GAT | TCT | 435 |  |
| Trp | Glu | Tyr | Ala | Phe | Glu | Gly | Thr | Xaa | Gly | Arg | Phe | Leu | Thr | Asp | Ser |     |  |
|     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |     |     |     |  |
| AGC | ATA | TGG | ATT | CAG | TGC | CTG | GAA |     |     |     |     |     |     |     |     | 459 |  |
| Ser | Ile | Trp | Ile | Gln | Cys | Leu | Glu |     |     |     |     |     |     |     |     |     |  |
|     |     |     | 125 |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

## (2) INFORMATION FOR SEQ ID NO: 224:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..399
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 6..344  
id H09880  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 408..454
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 355..401  
id H09880  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..399
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 56..395  
id H29351  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 393..432
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 391..430  
id H29351  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 65..369
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 41..345  
id H94779  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 118..455
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..338  
id N27248  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 122..399
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..278  
id T74091  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 393..434
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 273..314  
id T74091  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 346..408
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq SFLPSALVIWTS/A

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

```

ACTCCTTTTA GCATAGGGGC TTCGGCGCCA GCGGCCAGCG CTAGTCGGTC TGGTAAGTGC 60
CTGATGCCGA GTTCCGTCTC TCGCGTCTTT TCCTGGTCCC AGGCAAAGCG GASGNAGATC 120
CTCAAACGGC CTAGTGCTTC GCGCTTCCGG AGAAAATCAG CGGTCTAATT AATTCCTCTG 180
GTTTGTTGAA GCAGTTACCA AGAATCTTCA ACCCTTTCCC ACAAAGCTA ATTGAGTACA 240
CGTTCCTGTT GAGTACACGT TCCTGTTGAT TTACAAAAGG TGCAGGTATG AGCAGGTCTG 300
AAGACTAACA TTTTGTGAAG TTGTAAAACA GAAACCTGT TAGAA ATG TGG TGG TTT 357
 Met Trp Trp Phe
 -20

CAG CAA GGC CTC AGT TTC CTT CCT TCA GCC CTT GTA ATT TGG ACA TCT 405
Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser
 -15 -10 -5

GCT GCT TTC ATA TTT TCA TAC ATT ACT GCA GTA ACA CTC CAC CAT ATA 453
Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His Ile
 1 5 10 15

```

(2) INFORMATION FOR SEQ ID NO: 225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 11..277
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 29..295  
id AA041777  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 56..277
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..222  
id HSC1QB111  
est



## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 135..281  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 56..202  
                           id H10738  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 81..133  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 1..53  
                           id H10738  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 75..277  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 6..208  
                           id HSC2KE111  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 89..263  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
                           region 2..176  
                           id W24981  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 106..228  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.4  
                           seq PLIFSLWCSGVLL/HI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

```

AAGAGTGCGC GGRSATTGGG GCTTTCCAGC TCTCACAGAA CCTTCAGCAT CCCCAGCTGC 60
CGGTCTTGGC ATCTTCGAAG TAAGGAGAGT TTTAGATGCT TCTGG ATG TTC AAT GCT 117
 Met Phe Asn Ala
 -40

AGC ACC TTT ACA GAC TGG AGC AGC TCG ATT TTC TTC GTA TTT ACT TTC 165
Ser Thr Phe Thr Asp Trp Ser Ser Ser Ile Phe Phe Val Phe Thr Phe
 -35 -30 -25

AAG AGC AAG AAA AGT GCT GGG CTC CCA CTT ATT TTC TCC CTG TGG TGT 213
Lys Ser Lys Lys Ser Ala Gly Leu Pro Leu Ile Phe Ser Leu Trp Cys
 -20 -15 -10

TCC GGA GTT CTG CTC CAT ATC CAC CAG AAA GCT GGC GGC CCA CGG CTT 261

```

Ser Gly Val Leu Leu His Ile His Gln Lys Ala Gly Gly Pro Arg Leu  
-5 1 5 10

TGG CGC ATC CAT GGC GAG CAG  
Trp Arg Ile His Gly Glu Gln  
15

282

## (2) INFORMATION FOR SEQ ID NO: 226:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 155..334
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 98.3  
region 1..181  
id HSU90144  
vrt

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 218..328
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 90..200  
id T70246  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 128..216
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..89  
id T70246  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 170..328
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 50..208  
id T70127  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 219..328  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 62..171  
id AA114263  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 159..218  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..60  
id AA114263  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 222..308  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 13.4  
seq SLLLVQLLTPCSA/QF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

|             |             |             |             |             |             |     |
|-------------|-------------|-------------|-------------|-------------|-------------|-----|
| GACTCTTACT  | GTTTCTCATG  | GTGAGAAGAC  | AATATTGCT   | TTCTCTTTT   | CCTTTCTTCC  | 60  |
| GGATGAGAGG  | NTAAGCCATA  | ATAGAAAGAA  | TGGAGAATTA  | TTGATTGACC  | GTCTTTATTC  | 120 |
| TGTGGGCTCT  | GATTCTCCAA  | TGGGAATACC  | AAGGGATGGT  | TTTCATACT   | GGAACCCWWA  | 180 |
| GGTAAAGACA  | CTCAAGGACA  | GACATTTTGT  | GCAGAGCATA  | G ATG AAA   | ATG GCA AGT | 236 |
|             |             |             |             | Met Lys     | Met Ala Ser | -25 |
| TCC CTG GCT | TTC CTT CTG | CTC AAC TTT | CAT GTC TCC | CTC CTC TTG | GTC         | 284 |
| Ser Leu Ala | Phe Leu Leu | Leu Asn Phe | His Val Ser | Leu Leu Leu | Val         |     |
|             | -20         |             | -15         |             | -10         |     |
| CAG CTG CTC | ACT CCT TGC | TCA GCT CAG | TTT TCT GTG | CTT GGA CCT | CTG         | 332 |
| Gln Leu Leu | Thr Pro Cys | Ser Ala Gln | Phe Ser Val | Leu Gly Pro | Leu         |     |
|             | -5          |             | 1           |             | 5           |     |

(2) INFORMATION FOR SEQ ID NO: 227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 414 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 182..411  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                           region 1..230  
                           id C15003  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 182..411  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                           region 1..230  
                           id HUM407E11B  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 182..369  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 1..188  
                           id C15677  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 212..369  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                           region 26..183  
                           id HUM169E08B  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 274..399  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.2  
                           seq LLFDLVCHEFCQS/DD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

```

ACCAGGAACA TCCAGCTATT TATGATAGCA TTTGCTTCAT TATGTCAAGT TCAACAAATG 60
TTGACTTGCT GGTGAAGGTG GGGGAGGTTG TGGACAAGCT CTTTGATTTG GATGAGAAAC 120
TAATGTTAAG AATGGGTCAG AAATGGGGCT GCTCAGCCTC TGGACCAACC CCAGGAAGAG 180
TCTGAAGAGC AGCCAGTGTT TCGGCTTGTT CCCTGTATAC TTGAAGCTGC CAAACAAGTA 240
CGTTCTGAAA ATCCAGAATG GCTTGATGTT TAC ATG CAC ATT TTA CAA CTG CTT 294
 Met His Ile Leu Gln Leu Leu
 -40

ACT ACA GTG GAT GAT GGA ATT CAA GCA ATT GTA CAT TGT CCT GAC ACT 342
Thr Thr Val Asp Asp Gly Ile Gln Ala Ile Val His Cys Pro Asp Thr

```

|                                                                 |     |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|
| -35                                                             | -30 | -25 | -20 |     |
| GGA AAA GAC ATT TGG AAT TTA CTT TTT GAC CTG GTC TGC CAT GAA TTC |     |     |     | 390 |
| Gly Lys Asp Ile Trp Asn Leu Leu Phe Asp Leu Val Cys His Glu Phe |     |     |     |     |
|                                                                 | -15 | -10 | -5  |     |
| TGC CAG TCT GAT GAT CCA GCC CGG                                 |     |     |     | 414 |
| Cys Gln Ser Asp Asp Pro Ala Arg                                 |     |     |     |     |
|                                                                 | 1   | 5   |     |     |

## (2) INFORMATION FOR SEQ ID NO: 228:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..96
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..31  
id AA017364  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 114..242
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2  
seq PMQLLQVLSDVLA/EI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| AAACCGTTGC CAAGGAGCTC GACTCTGGGA GCGGTCTAGA GCCCCGGGCGC CTCCTGGGGG | 60  |
| GTGGGGAAAC GGTTCCTGA GGAGAATTTG AGTTAAAATT ATAAGACCTA ATT ATG      | 116 |
|                                                                    | Met |
| AGT GAT CAA ATT AAA TTC ATT ATG GAC AGT CTC AAT AAG GAG CCC TTT    | 164 |
| Ser Asp Gln Ile Lys Phe Ile Met Asp Ser Leu Asn Lys Glu Pro Phe    |     |
| -40 -35 -30                                                        |     |
| AGG AAG AAC TAT AAT TTA ATC ACG TTT GWT TCC TTG GAG CCA ATG CAA    | 212 |
| Arg Lys Asn Tyr Asn Leu Ile Thr Phe Xaa Ser Leu Glu Pro Met Gln    |     |
| -25 -20 -15                                                        |     |
| CTA TTA CAA GTT CTC AGT GAT GTT CTG GCT GAG ATT GAC CCA AAG CAA    | 260 |
| Leu Leu Gln Val Leu Ser Asp Val Leu Ala Glu Ile Asp Pro Lys Gln    |     |

|                                                                 |    |    |    |     |
|-----------------------------------------------------------------|----|----|----|-----|
| -10                                                             | -5 | 1  | 5  |     |
| CTT GTG GAT ATC AGA GAG GAG ATG CCA GAG CAG ACA GCC AAA CGA ATG |    |    |    | 308 |
| Leu Val Asp Ile Arg Glu Glu Met Pro Glu Gln Thr Ala Lys Arg Met | 10 | 15 | 20 |     |
| TTG AGC CTT CTT GGT ATT CTT AAG TAC AAA CCT TCA GGA AAT GCC ACA |    |    |    | 356 |
| Leu Ser Leu Leu Gly Ile Leu Lys Tyr Lys Pro Ser Gly Asn Ala Thr | 25 | 30 | 35 |     |
| GAT ATG AGT ACT TTT CGT CAG GGT TTG GTG ATT GGA AGT AAA CCT GTA |    |    |    | 404 |
| Asp Met Ser Thr Phe Arg Gln Gly Leu Val Ile Gly Ser Lys Pro Val | 40 | 45 | 50 |     |
| ATT TAC CCA GTG CTC                                             |    |    |    | 419 |
| Ile Tyr Pro Val Leu                                             |    |    |    |     |
| 55                                                              |    |    |    |     |

## (2) INFORMATION FOR SEQ ID NO: 229:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..203
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..151  
id T34361  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 205..358
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 152..305  
id T34361  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 205..342
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 131..268  
id HSC16A051  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 74..203
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 1..130  
id HSC16A051  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 340..373
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 267..300  
id HSC16A051  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 41..236  
id T35252  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 255..302
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 236..283  
id T35252  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..146
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 57..143  
id H92421  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 205..278
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 200..273  
id H92421  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..203
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 85..227

id T19059

est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 205..270  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
 region 228..293  
 id T19059  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 93..329  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.6  
 seq IIHAXGLVRECLA/XT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

```

AAGACCTGGG CGTCTGGAAT GATCTACGTG CTAAATACA CCACTCGCCA CCATTTTCTC 60
CAGCTGGGAG TGTCCACTCG CCTTCCACCA GC ATG GCA ACG TCK TCA CAG KAC 113
 Met Ala Thr Ser Ser Gln Xaa
 -75

CGC CAG CTG CTC AGT GAC TAC GGG CCA CCG TCC CTA GGC TAC ACC CAG 161
Arg Gln Leu Leu Ser Asp Tyr Gly Pro Pro Ser Leu Gly Tyr Thr Gln
 -70 -65 -60

GGA ACT GGG AAC AGC CAR RTG CCC CAA AGC AAA TAC GCG GAG CTG CTG 209
Gly Thr Gly Asn Ser Gln Xaa Pro Gln Ser Lys Tyr Ala Glu Leu Leu
 -55 -50 -45

GCC ATC ATT GRA GAG CTG GGG AAG GAG ATC AGA CCC ATG TAC GCA GGG 257
Ala Ile Ile Xaa Glu Leu Gly Lys Glu Ile Arg Pro Met Tyr Ala Gly
 -40 -35 -30 -25

AGC AAG AGT GCC ATG GAG AGG CTG AAG CGC GGC ATC ATT CAC GCT MSA 305
Ser Lys Ser Ala Met Glu Arg Leu Lys Arg Gly Ile Ile His Ala Xaa
 -20 -15 -10

GGM CTR GTT CGG GAG TGC TTG GCA GAM ACG GAA CGA ATG CCA GAT CCT 353
Gly Leu Val Arg Glu Cys Leu Ala Xaa Thr Glu Arg Met Pro Asp Pro
 -5 1 5

AGC TGC CTT GTT GGT TTT 371
Ser Cys Leu Val Gly Phe
 10

```

## (2) INFORMATION FOR SEQ ID NO: 230:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR



(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 107..234
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..128  
id N88564  
est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 59..103
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5  
seq LLGAAVAALGRG/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

```
AACCGGCAGC TGAACCCACC CGGCGCCACG GGACTTTGAC GCGTGCTCTG CGCTTGCC 58
ATG AGA CTC CTG GGA GCT GCA GCC GTC GCG GCT CTG GGG CGC GGA AGG 106
Met Arg Leu Leu Gly Ala Ala Ala Val Ala Ala Leu Gly Arg Gly Arg
-15 -10 -5 1
GCC CCC GCC TCC CTA GGC TGG CAG AGG AAG CAG GTT AAT TGG AAG GCC 154
Ala Pro Ala Ser Leu Gly Trp Gln Arg Lys Gln Val Asn Trp Lys Ala
 5 10 15
TGC CGA TGG TCT TCA TCA GGG GTG ATT CCT AAT GAA AAA ATA CGA AAT 202
Cys Arg Trp Ser Ser Ser Gly Val Ile Pro Asn Glu Lys Ile Arg Asn
 20 25 30
ATT GGA ATC TCA GCT CAC ATT GAT TCT GGG AAG 235
Ile Gly Ile Ser Ala His Ile Asp Ser Gly Lys
 35 40
```

(2) INFORMATION FOR SEQ ID NO: 231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 13..162  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 20..169  
                           id N41898  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 26..162  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 38..174  
                           id H69272  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 45..162  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 1..118  
                           id N20619  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 13..60  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.5  
                           seq RLLLRFLASVIS/RK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AATTGCAGGG AG ATG GCT CAG CGA CTT CTT CTG AGG AGG TTC CTG GCC TCT | 51  |
| Met Ala Gln Arg Leu Leu Leu Arg Arg Phe Leu Ala Ser               |     |
| -15 -10 -5                                                        |     |
| GTC ATC TCC AGG AAG CCC TCT CAG GGT CAG TGG CCA CCC CTC ACT TCC   | 99  |
| Val Ile Ser Arg Lys Pro Ser Gln Gly Gln Trp Pro Pro Leu Thr Ser   |     |
| 1 5 10                                                            |     |
| AGA GCC CTG CAG ACC CCA CAA TGC AGT CCT GGT GGC CTG ACT GTA ACA   | 147 |
| Arg Ala Leu Gln Thr Pro Gln Cys Ser Pro Gly Gly Leu Thr Val Thr   |     |
| 15 20 25                                                          |     |
| CCC AAC CCA GCG CCG GGG                                           | 165 |
| Pro Asn Pro Ala Pro Gly                                           |     |
| 30 35                                                             |     |

## (2) INFORMATION FOR SEQ ID NO: 232:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 base pairs  
 (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 59..214  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..156  
id AA069390  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 122..169  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.4  
seq LNSLSALAEELAVG/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

```
AAGGAGAGTC ACGTGAGAGT GGGCGGAGGG GGTGGAGGTT TGTCTCCGCT GTTTCATCTC 60
TATGGCTGTC AGAGGTGGGC GGCTTTGACC GAGAGGCTGC TGGAGCTCGT GTTTGGACGC 120
G ATG TTT CGT CTG AAC TCA CTT TCT GCT TTG GCA GAA CTG GCT GTG GGT 169
 Met Phe Arg Leu Asn Ser Leu Ser Ala Leu Ala Glu Leu Ala Val Gly
 -15 -10 -5

TCT CGA TGG TAC CAT GGA GGA TCA CAG CCC ATC CAG ATC CGG CTA GCG 217
Ser Arg Trp Tyr His Gly Gly Ser Gln Pro Ile Gln Ile Arg Leu Ala
 1 5 10 15
```

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 358 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 44..169  
(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 1..126  
id AA094226  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 170..231  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 126..187  
id AA094226  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 230..261  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 185..216  
id AA094226  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 44..195  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 129..280  
id R13710  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 193..254  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 279..340  
id R13710  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 44..282  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 172..410  
id R54574  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 44..184  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 159..299  
id T78111  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 182..222  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 298..338  
                           id T78111  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 220..254  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 337..371  
                           id T78111  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 89..271  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.9  
                           seq YTAVSVLAGPRWA/DP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

```

GCGGCGCGGC CGTAAAGCGC CATTACGCAG AGAGAAAGTT ACGAGAACT CGTTTTTCATC 60
TTCTTGGTTT CATCTTAATA CCAACGTC ATG TCT GGT TCT AAT GGT TCC AAA 112
 Met Ser Gly Ser Asn Gly Ser Lys
 -60 -55

GAA AAT TCT CAC AAT AAG GCT CGG ACG TCT CCT TAC CCA GGT TCA AAA 160
Glu Asn Ser His Asn Lys Ala Arg Thr Ser Pro Tyr Pro Gly Ser Lys
 -50 -45 -40

GTT GAA CGA AGC CAG GTT CCT AAT GAG AAA GTG GGC TGG CTT GTT GAG 208
Val Glu Arg Ser Gln Val Pro Asn Glu Lys Val Gly Trp Leu Val Glu
 -35 -30 -25

TGG CAA GAC TAT AAG CCT GTG GAA TAC ACT GCA GTC TCT GTC TTG GCT 256
Trp Gln Asp Tyr Lys Pro Val Glu Tyr Thr Ala Val Ser Val Leu Ala
 -20 -15 -10

GGA CCC AGG TGG GCA GAT CCT CAG ATC AGT GAA AGT AAT TTT TCT CCC 304
Gly Pro Arg Trp Ala Asp Pro Gln Ile Ser Glu Ser Asn Phe Ser Pro
 -5 1 5 10

AAG TTT AAC GAA AAG GAT GGG CAT GTT GAG AGA AAG AGC AAG AAT GGC 352
Lys Phe Asn Glu Lys Asp Gly His Val Glu Arg Lys Ser Lys Asn Gly
 15 20 25

CTG TAT 358
Leu Tyr

```

## {2} INFORMATION FOR SEQ ID NO: 234:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 base pairs

(B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 294..347  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
                                   region 297..350  
                                   id AA038489  
                                   est

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 134..347  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                                   region 1..214  
                                   id AA111922  
                                   est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 284..331  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.5  
                                   seq TLMFSLTAQWXTS/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

```

AAAAAAAAGC TGCTGGACCC CAGGGAGAGC TGACCACTGC CCGAGCAGCC GGCTGAATCC 60
ACCTCCACAA TGCSGCTCTC AGGAACCCCG GYCCCTAATA AGAAGAGGAA ATCCAGCAAG 120
CTGATCATGG AACTCACTGG AGGTGGACAG GAGAGCTCAG GCTTGAACCT GGGCAAAAAG 180
ATCAGTGTCC CAAGGGATGT GATGTTGGAG GAACTGTCGC TGCTTACCAA CCGGGGCTCC 240
AAGATGTTCA AACTGSGGCA GATGAGGGTG GAGAAGTTTA TTT ATG AGA ACC ACC 295
 Met Arg Thr Thr
 -15

CTG ATG TTT TCT CTG ACA GCT CAA TGG WTC ACT TCC AGA AGT TCC TTC 343
Leu Met Phe Ser Leu Thr Ala Gln Trp Xaa Thr Ser Arg Ser Ser Phe
 -10 -5 1

CAA
Gln
5
 346

```

(2) INFORMATION FOR SEQ ID NO: 235:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..384
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 8..357  
id H11129  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 43..346
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 16..319  
id R11829  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..302
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..253  
id R18811  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 302..366
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 254..318  
id R18811  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 183..371
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 6..194  
id R10511  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide

(B) LOCATION: 73..147  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 14.1  
 seq LTLTLLTLLAFA/GY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

```

ACTGCGCGGA TCGGCGTCCG CAGCGGGCGG CTGCTGAGCT GCCTTGAGGT GCAGTGTTGG 60
GGATCCAGAG CC ATG TCG GAC CTG CTA CTA CTG GGC CTG ATT GGG GGC CTG 111
 Met Ser Asp Leu Leu Leu Leu Gly Leu Ile Gly Gly Leu
 -25 -20 -15

ACT CTC TTA CTG CTG CTG ACG CTG CTG GCC TTT GCC GGG TAC TCA GGG 159
Thr Leu Leu Leu Leu Leu Thr Leu Leu Ala Phe Ala Gly Tyr Ser Gly
 -10 -5 1

CTA CTG GCT GGG GTG GAA GTG AGT GCT GGG TCA CCC CCC ATC CGC AAC 207
Leu Leu Ala Gly Val Glu Val Ser Ala Gly Ser Pro Pro Ile Arg Asn
 5 10 15 20

GTC ACT GTG GCC TAC AAG TTC CAC ATG GGG CTC TAT GGT GAG ACT GGG 255
Val Thr Val Ala Tyr Lys Phe His Met Gly Leu Tyr Gly Glu Thr Gly
 25 30 35

CGG CTT TTC ACT GAG AGC TGC AGC ATC TCT CCC AAG CTC CGC TCC ATC 303
Arg Leu Phe Thr Glu Ser Cys Ser Ile Ser Pro Lys Leu Arg Ser Ile
 40 45 50

GCT GTC TAC TAT GAC AAC CCC CAC ATG GTG CCC CCT GAT AAG TGC CGA 351
Ala Val Tyr Tyr Asp Asn Pro His Met Val Pro Pro Asp Lys Cys Arg
 55 60 65

TGT GCC GTG GGC AGC ATC CTG AGT GAA GGT GAG 384
Cys Ala Val Gly Ser Ile Leu Ser Glu Gly Glu
 70 75

```

(2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 75..218
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 29..172  
id T64530



est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 36..131
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.4  
seq LWSLALWLPLALS/VS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

```

AATCCGGACT GATAACCAGC CGGCCAGACT GAGGG ATG GAA GGC ACT GAG ATG 53
 Met Glu Gly Thr Glu Met
 -30

GGG GCC CGT CCA GGC GGA CAC CCG CRG AAA TGG AGC TTT CTG TGG TCT 101
Gly Ala Arg Pro Gly Gly His Pro Xaa Lys Trp Ser Phe Leu Trp Ser
-25 -20 -15

CTT GCA CTC TGG CTG CCT CTT GCC CTC TCT GTG TCT CTC TTT CTT GGT 149
Leu Ala Leu Trp Leu Pro Leu Ala Leu Ser Val Ser Leu Phe Leu Gly
-10 -5 1 5

CTC TCC CTC TCT CCT CCT CAG CCT GGT CTT TCT CTT TGG TGC ACA CTT 197
Leu Ser Leu Ser Pro Pro Gln Pro Gly Leu Ser Leu Trp Cys Thr Leu
 10 15 20

AGT TAT TGT TGT GAG CAA TGG AAG TTC AAA GGA ACT CCC TCT CCA GCT 245
Ser Tyr Cys Cys Glu Gln Trp Lys Phe Lys Gly Thr Pro Ser Pro Ala
 25 30 35

CTT CTG AAT CTK GGG ACA CGC GGG 269
Leu Leu Asn Leu Gly Thr Arg Gly
40 45

```

## (2) INFORMATION FOR SEQ ID NO: 237:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 220..396
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 207..383  
id N28787  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 108..207
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 95..194  
id N28787  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 220..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 209..305  
id AA019783  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 108..207
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 97..196  
id AA019783  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 307..392
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 297..382  
id AA019783  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 108..207
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 99..198  
id H86396  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 307..374
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 300..367  
id H86396  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 255..313
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 247..305

id H86396  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 220..336  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 210..326  
id H86516  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 108..207  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 98..197  
id H86516  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 327..368  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 318..359  
id H86516  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 108..207  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 111..210  
id AA059290  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 272..354  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 285..367  
id AA059290  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 220..286  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 223..289  
id AA059290  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 139..302  
(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 11.2  
seq LLFALGSLGLIFA/LI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

```

ARCGGTTAGT GGACCGGGAC CGGTAVGGGT GCTGTWGCCA TCATGGCTGA CCCCMMCCC 60
CGGBACMCTC GCTCCTCGAT CGAGGACGAC TTCANMTMNG GCAGGCAAGC GTGGCCTCCG 120
CCACCGTGYM BNTCCGA ATG VCC TTT CTG AGA AAA GTC TMN AGC ATT CTT 170
 Met Xaa Phe Leu Arg Lys Val Xaa Ser Ile Leu
 -55 -50 -45

TCT CTG CAG GTT CTC TTA ACT ACA GTG ACT TCA ACA GTT TTT TTA TAC 218
Ser Leu Gln Val Leu Leu Thr Thr Val Thr Ser Thr Val Phe Leu Tyr
 -40 -35 -30

TTT GAG TCT GTA CGG ACA TTT GTA CMT GAG AGT CCT GCC TTA ATT TTG 266
Phe Glu Ser Val Arg Thr Phe Val Xaa Glu Ser Pro Ala Leu Ile Leu
 -25 -20 -15

CTG TTT GCC CTC GGA TCT CTG GGT TTG ATT TTT GCG TTG ATT TTA AAC 314
Leu Phe Ala Leu Gly Ser Leu Gly Leu Ile Phe Ala Leu Ile Leu Asn
 -10 -5 1

AGV CAT AAG TAT CCC CTT AAC CTG TAC CTA CTT TTT GGA TTT ACG CTG 362
Xaa His Lys Tyr Pro Leu Asn Leu Tyr Leu Leu Phe Gly Phe Thr Leu
 5 10 15 20

TTG GMA GCT CTG ACT GTG GCA GTT GTT GTT ACT 395
Leu Xaa Ala Leu Thr Val Ala Val Val Val Thr
 25 30

```

(2) INFORMATION FOR SEQ ID NO: 238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..155
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 24..126  
id AA075942  
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 66..136  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 37..107  
id AA262924  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 22..135  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 10.8  
seq MLLLLLLLGSQG/PQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AAAGGGTCGT TGGTGGGAAA G ATG GCG GCG ACT CTG GGA CCC CTT GGG TCG | 51  |
| Met Ala Ala Thr Leu Gly Pro Leu Gly Ser                         |     |
| -35 -30                                                         |     |
| TGG CAG CAG TGG CGG CGA TGT TTG TCG GCT CGG GAT GGG TCC AGG ATG | 99  |
| Trp Gln Gln Trp Arg Arg Cys Leu Ser Ala Arg Asp Gly Ser Arg Met |     |
| -25 -20 -15                                                     |     |
| TTA CTC CTT CTT CTT TTG TTG GGG TCT GGG CAG GGG CCA CAG CAA GTC | 147 |
| Leu Leu Leu Leu Leu Leu Gly Ser Gly Gln Gly Pro Gln Gln Val     |     |
| -10 -5 1                                                        |     |
| GGG GCG GGG                                                     | 156 |
| Gly Ala Gly                                                     |     |
| 5                                                               |     |

(2) INFORMATION FOR SEQ ID NO: 239:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(64..95)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 79..110  
id N98118  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 195..317  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 9.9  
 seq ILPFLLPFPVNA/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

```

ATAGTGATCC TTTTCCTTCT CCCACTCCGT AAGTTTCTAT CCTTGGCCTC CTATTCTTTT 60
TACTACATAT ATACTTTATA TATACATATA TACTTGGAAC AGGCTTAATG AGTTCCAAGG 120
TTTCAAGTAT AATAGAAGGA TAGTTTCCCT AATATTTCTT CAAAACAGAT TTCTCTTCTG 180
AAATCCAGAG TCAT ATG TCC AGT TGG ATG TAT CTT GGA TAC CCC ATT GTC 230
 Met Ser Ser Trp Met Tyr Leu Gly Tyr Pro Ile Val
 -40 -35 -30
ACC TCA AAC ACT ACT TGT CTA AAA CTG ATC TCA TCA TCT TTT CCC CAA 278
Thr Ser Asn Thr Thr Cys Leu Lys Leu Ile Ser Ser Ser Phe Pro Gln
 -25 -20 -15
ATC CTT CCT TTT CTT CTA TTT CCC TTC CCA GTG AAT GCC AGA TCT CAC 326
Ile Leu Pro Phe Leu Leu Phe Pro Phe Pro Val Asn Ala Arg Ser His
 -10 -5 1
TYA GTT GCT CAA ACT AAA AGC CCG AGG 353
Xaa Val Ala Gln Thr Lys Ser Pro Arg
 5 10

```

(2) INFORMATION FOR SEQ ID NO: 240:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 88..132  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 352..396  
 id AA021024  
 est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 46..108  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 9.7  
 seq QLCLLLLPSCSLS/VS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

```

ACCTCTTGGG GCCTACTTTG GGATGAAGTR GCCTCCCTCA GCAGC ATG GCC CCT GGG 57
 Met Ala Pro Gly
 -20

GTC ATC ATC ATC CAG CTC TGC CTC TTG CTC CTG CCT TCC TGC TCC CTT 105
Val Ile Ile Ile Gln Leu Cys Leu Leu Leu Leu Pro Ser Cys Ser Leu
 -15 -10 -5

TCT GTT TCC GGA TGT TCC TGC CCT AGT GCC TGC TTC AGC ACC ACC AGC 153
Ser Val Ser Gly Cys Ser Cys Pro Ser Ala Cys Phe Ser Thr Thr Ser
 1 5 10 15

CGC GAG 159
Arg Glu

```

(2) INFORMATION FOR SEQ ID NO: 241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 283..322
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 179..218  
id N78639  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 283..322
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 193..232  
id AA150442  
est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 99..377
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.6  
seq LSLSLGASAPVQC/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

```

ACATGCTCAG GGTGAGGTTT CAGCCCCAGC TGAGGGCTGA GGGGAGTGGG TGGACATGGG 60
GCAGGGAGCT GGAAGAACAC TCGAGAGACA GCAGGTAG ATG AGA CAT GGC TTT ATT 116
 Met Arg His Gly Phe Ile
 -90

CAG CAG CAG TTT TCA TTA ACA GCT TTC TCA MAC STT WRG SCW ATC TTC 164
Gln Gln Gln Phe Ser Leu Thr Ala Phe Ser Xaa Xaa Xaa Xaa Ile Phe
 -85 -80 -75

ACA CTG KST GSC CTG TCT CAG TTG CTT AGT TCA GCA GCT CCC AAA CAC 212
Thr Leu Xaa Xaa Leu Ser Gln Leu Leu Ser Ser Ala Ala Pro Lys His
 -70 -65 -60

ACA GCT GCA CCG ACG GCC CTC CCT TGC CTT CAG GGT CAG CAG CTT AAC 260
Thr Ala Ala Pro Thr Ala Leu Pro Cys Leu Gln Gly Gln Gln Leu Asn
 -55 -50 -45 -40

TCT CTC TCT CTG GGC ACA AGT GAG CTG AGC TGT GTC CTG GCT TCC TCC 308
Ser Leu Ser Leu Gly Thr Ser Glu Leu Ser Cys Val Leu Ala Ser Ser
 -35 -30 -25

TGT CTA TCT ACA AAG ACA GAC CCC TCT GGT CTC TCT CTC TCT TTG GGT 356
Cys Leu Ser Thr Lys Thr Asp Pro Ser Gly Leu Ser Leu Ser Leu Gly
 -20 -15 -10

GCC AGC GCA CCT GTA CAG TGT CAG CAG GAC AAT TAT ACC TTT TGC KNN 404
Ala Ser Ala Pro Val Gln Cys Gln Gln Asp Asn Tyr Thr Phe Cys Xaa
 -5 1 5

CAA TAC TGG CTT AGA GCA AGG CAT 428
Gln Tyr Trp Leu Arg Ala Arg His
 10 15

```

(2) INFORMATION FOR SEQ ID NO: 242:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 325..371
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 277..323  
id AA015589



est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 325..371
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 277..323  
id AA019963  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 140..262
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.5  
seq LIIFLSFLPFINS/SF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

```

ACAAGTGGGA TAGGTCCTGT GACAGAATTG TGTGATACAG GTCAAACAGG AGTTGGGTTA 60
TGGGGAAAAT GCCAGTTGAA ATATGTTTTG ATCTTTGGAG AAACCTATTT TTTCATTTAA 120
CCTGTTCTTT AAATCCAGT ATG TTC CAG AAC ATA CAA AAA TGT TTA AAT GTT 172
 Met Phe Gln Asn Ile Gln Lys Cys Leu Asn Val
 -40 -35

CCA TTT GTA AGA GGA TAT CAT GTA TTT TAT ATC AAT TTA AAT GCA GTT 220
Pro Phe Val Arg Gly Tyr His Val Phe Tyr Ile Asn Leu Asn Ala Val
-30 -25 -20 -15

ATC CTA ATC ATT TTT CTT TCA TTT TTA CCC TTT ATT AAC TCT TCA TTT 268
Ile Leu Ile Ile Phe Leu Ser Phe Leu Pro Phe Ile Asn Ser Ser Phe
 -10 -5 1

GTT TAC AAA ACA AAT CCA CTC TAT GAC GCA ATC TCT AAT TAT GTG TTT 316
Val Tyr Lys Thr Asn Pro Leu Tyr Asp Ala Ile Ser Asn Tyr Val Phe
 5 10 15

TCT TTC AGG TAT CCA AAC CTT GRA ASC TTT GCT CTA GAT GTC AGG CTT 364
Ser Phe Arg Tyr Pro Asn Leu Xaa Xaa Phe Ala Leu Asp Val Arg Leu
 20 25 30

GTT TTT
Val Phe
35

```

## (2) INFORMATION FOR SEQ ID NO: 243:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(215..358)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 165..308  
id R98055  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 185..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 252..356  
id W23510  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 136..186
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 202..252  
id W23510  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 73..109
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 139..175  
id W23510  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 315..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 385..422  
id W23510  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(215..358)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 144..287  
id T46976  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: complement(227..358)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                           region 167..298  
                           id AA084768  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(248..358)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 169..279  
                           id R50108  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(215..250)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
                           region 278..313  
                           id R50108  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 281..340  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 9.2  
                           seq FPVLALFLSGSLA/LF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

```

AGAGTGAGAC GGGCAGATGG AGGAGGGATT GTAATGGCGG YAGCGGCAGC TCCCSTGCTC 60
TGACCCACGG CAGGCATACA GCATCCGATT TAATCTGGAT CCATTCCGGC GCCTTCCTCT 120
CCCAGTCACC CAGAGGGCCC CAACCCCGGC GGCCCTTTCT TCCTCAAATG TCCTCGGCTC 180
TATACCGTGC CTGGGTCTTT TCTCTTTCTC TCTGCCTGGA AGATTCCTTC TTTCCCCTTT 240
TGTCTTGCCC ACTCCTGTTT ACCCTTCAAG TTTCAAGTTC ATG TCA CTG TCT CAG 295
 Met Ser Leu Ser Gln
 -20

AGA GGT TTT CCT GTG CTC GCC CTG TTT CTC TCA GGA AGC CTT GCT CTT 343
Arg Gly Phe Pro Val Leu Ala Leu Phe Leu Ser Gly Ser Leu Ala Leu
-15 -10 -5 1

TTC CAT CAT ACC TCT GGG
Phe His His Thr Ser Gly
 5

```

## (2) INFORMATION FOR SEQ ID NO: 244:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 268 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..132
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..114  
id N87112  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 194..267
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 174..247  
id N87112  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 130..195
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 111..176  
id N87112  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 68..267
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..200  
id T68050  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..209
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 1..147  
id AA157180  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..195
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 1..130  
id AA094982  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 190..264  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 5..79  
id W00395  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 59..145  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.9  
seq ALLIVCDVPSASA/QR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ACCCACCTC AGACCTAGCC GGAGCAAAGT TTCACTTATA GAAGGGAGAG AAGCGAAC  | 58  |
| ATG GCA GCG CGT TGG CGG TTT TGG TGT GTC TCT GTG ACC ATG GTG GTG | 106 |
| Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val Val |     |
| -25 -20 -15                                                     |     |
| GCG CTG CTC ATC GTT TGC GAC GTT CCC TCA GCC TCT GCC CAA AGA AAG | 154 |
| Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln Arg Lys |     |
| -10 -5 1                                                        |     |
| AAG GAG ATG GTG TTA TCT GAA AAG GTT AGT CAG CTG ATG GAA TGG ACT | 202 |
| Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met Glu Trp Thr |     |
| 5 10 15                                                         |     |
| AAC AAA AGA CCT GTA ATA AGA ATG AAT GGA GAC AAG TTC CGT CGC CTT | 250 |
| Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys Phe Arg Arg Leu |     |
| 20 25 30 35                                                     |     |
| GTG AAA GMN CCA CCG AGG                                         | 268 |
| Val Lys Xaa Pro Pro Arg                                         |     |
| 40                                                              |     |

## (2) INFORMATION FOR SEQ ID NO: 245:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 131..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 45..241  
id H81225  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 86..123
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..38  
id H81225  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 2..208  
id W01412  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 129..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..199  
id AA044118  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 131..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 13..209  
id W42797  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 209..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 95..213  
id R39635  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 130..209
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 15..94

id R39635  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 191..286
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8  
seq VPMLLLIVGGSFG/LR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

```
AACAAGTATG TTACGATGGC TCGATTGCTT TTGCCTAGCG GAAACCATTC ACTAAGGACC 60
GAGCACCAAA TAACCAAGGA AAAGGAAGTG AGTTAAGGAC GTACTCGTCT TGGTGAGAGC 120
GTGAGCTGCT GAGATTTGGG AGTCTGCGCT AGGCCCGCTT GGAGTTCTGA GCCGATGGAA 180
GAGTTCACTC ATG TTT GCA CCC GCG GTG ATG CGT GCT TTT CGC AAG AAC 229
 Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn
 -30 -25 -20

AAG ACT CTC GGC TAT GGA GTC CCC ATG TTG TTG CTG ATT GTT GGA GGT 277
Lys Thr Leu Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly
 -15 -10 -5

TCT TTT GGT CTT CGT GAG TTT TCT CNA ATC CGA TAT GAT GCT GTG AAG 325
Ser Phe Gly Leu Arg Glu Phe Ser Xaa Ile Arg Tyr Asp Ala Val Lys
 1 5 10

GGG
Gly 328
```

## (2) INFORMATION FOR SEQ ID NO: 246:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 106..210
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 104..208  
id AA131932  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 298..342  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 293..337  
id AA131932  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 86..291  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 67..272  
id AA001989  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 29..102  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 11..84  
id AA001989  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 102..331  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 76..305  
id W32996  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 55..96  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 31..72  
id W32996  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 236..377  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 165..306  
id AA121218  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 106..235  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 34..163  
id AA121218  
est



## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 70..180
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.5  
seq LLVLLLYAPVGFC/LL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

```

AAGAGCSSCT GCGGCCGGGC GCGAAAATGG CGGCGGCGGC GACGGCCNGG CGCTCCTGAA 60
GCAGCAGTT ATG GAG CTT CCC TCA GGG CCG GGG CCG GAG CGG CTC TTT GAC 111
 Met Glu Leu Pro Ser Gly Pro Gly Pro Glu Arg Leu Phe Asp
 -35 -30 -25

TCG CAC CGG CTT CCG GGT GAC TGC TTC CTA CTG CTC GTG CTG CTG CTC 159
Ser His Arg Leu Pro Gly Asp Cys Phe Leu Leu Leu Val Leu Leu Leu
 -20 -15 -10

TAC GCG CCA GTC GGG TTC TGC CTC CTC GTC CTG SGC CTC TTT CTC GGG 207
Tyr Ala Pro Val Gly Phe Cys Leu Leu Val Leu Xaa Leu Phe Leu Gly
 -5 1 5

ATC CAC GTC TTC CTG GTC AGC TGC GCG CTG CCA GAC AGC GTC CTT CGC 255
Ile His Val Phe Leu Val Ser Cys Ala Leu Pro Asp Ser Val Leu Arg
 10 15 20 25

AGA TTC GTA GTG CGG ACC ATG TGT GCG GTG CTA GGG CTC GTG GCC CGG 303
Arg Phe Val Val Arg Thr Met Cys Ala Val Leu Gly Leu Val Ala Arg
 30 35 40

CAG GAG GAC TCC GGA CTC CGG GAT CAC AGT GTC AGG GTC CTC ATT TCC 351
Gln Glu Asp Ser Gly Leu Arg Asp His Ser Val Arg Val Leu Ile Ser
 45 50 55

AAC CAT GTG ACA CCT TTC GAC CAC CAG 378
Asn His Val Thr Pro Phe Asp His Gln
 60 65

```

## (2) INFORMATION FOR SEQ ID NO: 247:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 38..181
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97  
region 1..144  
id W60505  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 186..312  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 150..276  
id W60505  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 305..346  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 270..311  
id W60505  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 38..312  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 1..275  
id W60589  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 305..346  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 269..310  
id W60589  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 32..175  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..144  
id R33763  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 176..261  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 144..229  
id R33763  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 268..312  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 238..282  
id R33763  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 305..337  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 276..308  
id R33763  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 33..176  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 3..146  
id AA123856  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 181..346  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 88..253  
id HSB31E112  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 93..181  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 1..89  
id HSB31E112  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 106..375  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.4  
seq SLVLLTVTPSXRQ/QE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

AGGACTTCCC CCGGGCTGAG CTGCGCASGG GGTTTTGGCC AAATTGGGCG AGGGCACAAA 60

ATAACCACTT ACCCCTTCTC ACCGAGGAAG AGCGGGAGAA AGGGT ATG GCA CAG TCA 117  
Met Ala Gln Ser  
-90

CPA GGS TGG GTG RAA AGR TAC KTC AAG GCC TTT TGT AAA GGC TTC TTT 165  
Gln Gly Trp Val Xaa Arg Tyr Xaa Lys Ala Phe Cys Lys Gly Phe Phe

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| -85                                                             | -80 | -75 |     |
| GTG GCG GTG CCT GTG GCA GTG ACT TTC TTG GAT CGG GTC GCC TGT GTG | 213 |     |     |
| Val Ala Val Pro Val Ala Val Thr Phe Leu Asp Arg Val Ala Cys Val |     |     |     |
| -70                                                             | -65 | -60 | -55 |
| GCA AGA GTA GAA GGA GCA TCG ATG CAG CCT TCT TTG AAT CCT GGG GGG | 261 |     |     |
| Ala Arg Val Glu Gly Ala Ser Met Gln Pro Ser Leu Asn Pro Gly Gly |     |     |     |
| -50                                                             | -45 | -40 |     |
| AGC NAG TCA TCT GAT GTG GTG SDD DTG AAC CAC TGG AAA GTG AGG AAT | 309 |     |     |
| Ser Xaa Ser Ser Asp Val Val Xaa Xaa Asn His Trp Lys Val Arg Asn |     |     |     |
| -35                                                             | -30 | -25 |     |
| TTT GAA GTA CAC CGT GGT GAC ATT GTA TCA TTG GTG TTG CTC ACT GTG | 357 |     |     |
| Phe Glu Val His Arg Gly Asp Ile Val Ser Leu Val Leu Leu Thr Val |     |     |     |
| -20                                                             | -15 | -10 |     |
| ACG CCC TCC ASC CGA CAA CAG GAG                                 | 381 |     |     |
| Thr Pro Ser Xaa Arg Gln Gln Glu                                 |     |     |     |
| -5                                                              | 1   |     |     |

## (2) INFORMATION FOR SEQ ID NO: 248:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 11..158
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 11..158  
id H56585  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 201..322
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 201..322  
id H56585  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 151..322
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93  
region 119..290  
id AA147898  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 39..159  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 8..128  
id AA147898  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 201..322  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 83..204  
id R52248  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 170..202  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 51..83  
id R52248  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 177..264  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 87..174  
id H54950  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 284..315  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 192..223  
id H54950  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(199..320)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 40..161  
id W22146  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 67..135  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 8.1  
 seq WLLVLSFVFGCNV/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

```

AGCCGCTGTT GTTGTGGTCC CCATGGAGCT GCCGTAGCGG ACCCAGCACA GCCAGGAGCG 60
TCCGGG ATG AGC TCA GCC GCG GCC GAC CAC TGG GCG TGG TTG CTG GTG 108
 Met Ser Ser Ala Ala Ala Asp His Trp Ala Trp Leu Leu Val
 -20 -15 -10
CTC AGC TTC GTG TTT GGA TGC AAT GTT CTT AGG ATC CTC CKC CCG GBC 156
Leu Ser Phe Val Phe Gly Cys Asn Val Leu Arg Ile Leu Xaa Pro Xaa
 -5 1 5
YTC STM ATC STG CAK GTC CAG GGT GCT GCA GAA GGA CGC GGA SAG GAG 204
Xaa Xaa Ile Xaa Xaa Val Gln Gly Ala Ala Glu Gly Arg Gly Xaa Glu
 10 15 20
TCA CAG ATG AGA GCG GAG ATC CAG GAC ATG AAG CAG GAG CTC TCC ACA 252
Ser Gln Met Arg Ala Glu Ile Gln Asp Met Lys Gln Glu Leu Ser Thr
 25 30 35
GTC AAC ATG ATG GAC GAG TTT GCC AGA TAT GCC AGG CTG GAN AGA AAG 300
Val Asn Met Met Asp Glu Phe Ala Arg Tyr Ala Arg Leu Xaa Arg Lys
 40 45 50 55
ATC AAC AAG ATG ACG GAT AAG
Ile Asn Lys Met Thr Asp Lys
 60

```

(2) INFORMATION FOR SEQ ID NO: 249:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 382 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 196..382  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
 region 10..196  
 id HSC2EA121  
 est

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 121..205  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 134..218  
                           id AA095017  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 197..252  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 209..264  
                           id AA095017  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 281..340  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 8  
                           seq HVFFLLLLAHIIA/LE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

```

GTTTTTGTGT GTGTGTGCGT GTTGTTGGCC TCCATCCCCA CTCCCCAGAC TCCACTTCTC 60
CAGGCCTCTC TCCCGCCTTT TCATCCCGCA TCCGCAGGAC ACCCAATCAC CGGGGCAACA 120
GGATGCCTTC CGCGCCTTCC ACCCTGACCT GGAATTCGTG GGCAAGTTCT TGAAACCCCT 180
GCTGATTGGT GAACTGGCCC CGGAGGAGCC CAGCCAGGAC CACGGCAAGA ACTCAAAGAT 240
CACTGAGGAC TTCCGGGCCC TGAGGAAGAC GGCTGAGGAC ATG AAC CTG TTC AAG 295
 Met Asn Leu Phe Lys
 -20

ACC AAC CAC GTG TTC TTC CTC CTC CTC CTG GCC CAC ATC ATC GCC CTG 343
Thr Asn His Val Phe Phe Leu Leu Leu Leu Ala His Ile Ile Ala Leu
-15 -10 -5 1

GAG AGC ATT GCA TGG TTC ACT GTC TTT TAC TTT GGC AAT 382
Glu Ser Ile Ala Trp Phe Thr Val Phe Tyr Phe Gly Asn
 5 10

```

## (2) INFORMATION FOR SEQ ID NO: 250:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 298 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 80..300
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 101..321  
id H21228  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..300
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 117..357  
id R72127  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..59
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 77..117  
id R72127  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..204
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 63..207  
id H18908  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 195..269
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 199..273  
id H18908  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..59
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 23..63  
id H18908  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 65..203
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95



region 144..282  
id W93461  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 19..59  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 98..138  
id W93461  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 252..288  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 333..369  
id W93461  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 228..259  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 308..339  
id W93461  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 136..300  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 93..257  
id HUM085F04B  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 170..241  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.9  
seq LLLPRVLLTMASG/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

|                                                                   |             |
|-------------------------------------------------------------------|-------------|
| AATCACGTGG CTGCCACCCA GGGGCATTCT TCGGGGGTGC ATCAGAGGGA GGGCAGAGCC | 60          |
| TGAGGATCTA AGCGAAGGCT TCCCCGGGTG TAATTCCTG GGCTGTTTGT GAGGAGAGAT  | 120         |
| CGAATTCGCC TCCTGCTCTC AGGCCTCTCT GCTCCTGTCT TTTGTTTGG ATG CCG GCG | 178         |
|                                                                   | Met Pro Ala |
| CTG CTG CCT GTG GCC TCC CGC CTT TTG TTG CTA CCC CGA GTC TTG CTG   | 226         |
| Leu Leu Pro Val Ala Ser Arg Leu Leu Leu Leu Pro Arg Val Leu Leu   |             |
| -20                                                               | -15         |
|                                                                   | -10         |

ACC ATG GCC TCT GGA AGC CCT CCG ACC CAG CCC TCG CCG GCC TCG GAT 274  
Thr Met Ala Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro Ala Ser Asp  
-5 1 5 10  
TCC GGC TCT GGC TAC GTT CCG GGC 298  
Ser Gly Ser Gly Tyr Val Pro Gly  
15

## (2) INFORMATION FOR SEQ ID NO: 251:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..286
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..286  
id HUM085F04B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 147..245
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 167..265  
id R64509  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 99..161
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 118..180  
id R64509  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 245..286
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 266..307  
id R64509  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 147..262
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 182..297  
id H85714  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 99..161
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 133..195  
id H85714  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 95..286
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 159..350  
id H21228  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 201..286
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 151..236  
id AA009893  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 148..206
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 97..155  
id AA009893  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 99..160
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 49..110  
id AA009893  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 1..198
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9  
seq LLLPRVLLTMASG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG ATA GGG TCG GGA TTG GCT GGC TCT GGA GGC GCA GGT GGT CCT TCT | 48  |
| Met Ile Gly Ser Gly Leu Ala Gly Ser Gly Gly Ala Gly Gly Pro Ser |     |
| -65 -60 -55                                                     |     |
| TCT ACT GTC ACA TGG TGC GCG CTG TTT TCT AAT CAC GTG GCT GCM ACC | 96  |
| Ser Thr Val Thr Trp Cys Ala Leu Phe Ser Asn His Val Ala Ala Thr |     |
| -50 -45 -40 -35                                                 |     |
| CAG GCC TCT CTG CTC CTG TCT TTT GTT TGG ATG CCG GCG CTG CTG CCT | 144 |
| Gln Ala Ser Leu Leu Leu Ser Phe Val Trp Met Pro Ala Leu Leu Pro |     |
| -30 -25 -20                                                     |     |
| GTG GCC TCC CGC CTT TTG TTG CTA CCC CGA GTC TTG CTG ACC ATG GCC | 192 |
| Val Ala Ser Arg Leu Leu Leu Leu Pro Arg Val Leu Leu Thr Met Ala |     |
| -15 -10 -5                                                      |     |
| TCT GGA AGC CCT CCG ACC CAG CCC TCG CCG GCC TCG GAT TCC GGC TCT | 240 |
| Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro Ala Ser Asp Ser Gly Ser |     |
| 1 5 10                                                          |     |
| GGC TAC GTT CCG GGC TCG GTC TCT GCA GCC TTT GTT ACT TGC CCC AGG | 288 |
| Gly Tyr Val Pro Gly Ser Val Ser Ala Ala Phe Val Thr Cys Pro Arg |     |
| 15 20 25 30                                                     |     |

(2) INFORMATION FOR SEQ ID NO: 252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 53..340  
id AA056366  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 80..367  
id R77008  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..223
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 77..268  
id W75983  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 223..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 269..365  
id W75983  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..223
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 129..320  
id W39055  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 223..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 321..417  
id W39055  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..236
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 84..288  
id N48534  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 264..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 318..373  
id N48534  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 11..82
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9  
seq LLLPRVLLTMASG/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATTGTGTTGG ATG CCG GCG CTG CTG CCT GTG GCC TCC CGC CTT TTG TTG  | 49  |
| Met Pro Ala Leu Leu Pro Val Ala Ser Arg Leu Leu Leu             |     |
| -20 -15                                                         |     |
| CTA CCC CGA GTC TTG CTG ACC ATG GCC TCT GGA AGC CCT CCG ACC CAG | 97  |
| Leu Pro Arg Val Leu Leu Thr Met Ala Ser Gly Ser Pro Pro Thr Gln |     |
| -10 -5 1 5                                                      |     |
| CCC TCG CCG GCC TCG GAT TCC GGC TCT GGC TAC GTT CCG GGC TCG GTC | 145 |
| Pro Ser Pro Ala Ser Asp Ser Gly Ser Gly Tyr Val Pro Gly Ser Val |     |
| 10 15 20                                                        |     |
| TCT GCA GCC TTT GTT ACT TGC CCC AAC GAG AAG GTC GCC AAG GAG ATC | 193 |
| Ser Ala Ala Phe Val Thr Cys Pro Asn Glu Lys Val Ala Lys Glu Ile |     |
| 25 30 35                                                        |     |
| GCC AGG GCC GTG GTG GAG AAG CGC CTA GCA GCC TGC GTC AAC CTC ATC | 241 |
| Ala Arg Ala Val Val Glu Lys Arg Leu Ala Ala Cys Val Asn Leu Ile |     |
| 40 45 50                                                        |     |
| CCT CAG ATT ACA TCC ATC TAT GAG TGG AAA GGG AHG ATC GAG GAA GAC | 289 |
| Pro Gln Ile Thr Ser Ile Tyr Glu Trp Lys Gly Xaa Ile Glu Glu Asp |     |
| 55 60 65                                                        |     |
| AGT GAG GTG CTG ATG ATG ATT AAA ACC CAA GCG                     | 322 |
| Ser Glu Val Leu Met Met Ile Lys Thr Gln Ala                     |     |
| 70 75 80                                                        |     |

## (2) INFORMATION FOR SEQ ID NO: 253:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 138..193
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 247..302  
id T80036  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 33..308

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7.6

seq FLLLTVALLASYS/VH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AAGATGGAAC TGGTAGTCAG CTGGAGAGCA GC ATG GAG GCG TCC TGG GGG AGC | 53  |
| Met Glu Ala Ser Trp Gly Ser                                     |     |
| -90                                                             |     |
| TTC AAC GCT GAG CGG GGC TGG TAT GTC TCT GTG CAG CAG CCT GAA GAA | 101 |
| Phe Asn Ala Glu Arg Gly Trp Tyr Val Ser Val Gln Gln Pro Glu Glu |     |
| -85 -80 -75 -70                                                 |     |
| GCG GAG GCC GAA GAG TTG AGT CCG TTG CTA AGC AAC GAA CTT CAC AGA | 149 |
| Ala Glu Ala Glu Glu Leu Ser Pro Leu Leu Ser Asn Glu Leu His Arg |     |
| -65 -60 -55                                                     |     |
| CAG CGA TCC CCA GGT GTT TCA TTT GGT TTA TCA GTG TTT AAT TTG ATG | 197 |
| Gln Arg Ser Pro Gly Val Ser Phe Gly Leu Ser Val Phe Asn Leu Met |     |
| -50 -45 -40                                                     |     |
| AAT GCC ATC ATG GGA AGT GGC ATC CTT GGC TTA GCT TAT GTT ATG GCT | 245 |
| Asn Ala Ile Met Gly Ser Gly Ile Leu Gly Leu Ala Tyr Val Met Ala |     |
| -35 -30 -25                                                     |     |
| AAT ACC GGT GTC TTT GGA TTT AGC TTC TTG CTG CTG ACA GTT GCT CTC | 293 |
| Asn Thr Gly Val Phe Gly Phe Ser Phe Leu Leu Leu Thr Val Ala Leu |     |
| -20 -15 -10                                                     |     |
| CTG GCT TCT TAC TCA GTC CAT CTT CTG CTT AGT ATG TGT ATT CAG ACA | 341 |
| Leu Ala Ser Tyr Ser Val His Leu Leu Leu Ser Met Cys Ile Gln Thr |     |
| -5 1 5 10                                                       |     |
| GCT GTA ACA TCT TAT GAA GAT CTT GGA CTC TTT GCA TTT GGA TTA CCT | 389 |
| Ala Val Thr Ser Tyr Glu Asp Leu Gly Leu Phe Ala Phe Gly Leu Pro |     |
| 15 20 25                                                        |     |
| GGA CTG                                                         | 395 |
| Gly Leu                                                         |     |

(2) INFORMATION FOR SEQ ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 18..132

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
                            region 1..115  
                            id T10447  
                            est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 78..128  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.6  
                            seq FFLLLRFFLRIDG/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

```
ATTTTGAAGA AGTTCTCCTT TTTGAGGATG AACTTCATGA TCATGGAGTT TCAAGCCTGA 60
GTGTGAAGAT TAGAGTA ATG CCT TCT AGC TTT TTC CTG CTG TTG CGG TTT 110
 Met Pro Ser Ser Phe Phe Leu Leu Leu Arg Phe
 -15 -10

TTC TTG AGA ATT GAC GGG GTG CCG 134
Phe Leu Arg Ile Asp Gly Val Pro
-5 1
```

(2) INFORMATION FOR SEQ ID NO: 255:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 337 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 44..276  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
                            region 1..233  
                            id N83601  
                            est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 51..276  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
                            region 15..240  
                            id N56180  
                            est

(ix) FEATURE:



(A) NAME/KEY: other  
(B) LOCATION: 69..216  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 23..170  
id R57553  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 46..75  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..30  
id R57553  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 58..142  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 42..126  
id R57171  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 18..56  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 1..39  
id R57171  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 142..182  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 97..137  
id N88966  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 49..83  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..35  
id N88966  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 200..256  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.6  
seq FIVGIYFLSSCRA/EE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

```

AGTCTTTGTC CTGAGCCCAC GATTCCAGAG CTGGCTGGAC CCAAGGAGGT GAAGAGTCAC 60
TTTTCAGCCC CAGGAAGGGC AAAGAAGAGA GARAATCAGC CTGTCTGCTC TCTCCTTGGC 120
TCAACAAGGC CTCTAACAGT CTTCTGTCCT CTATTCTGCA CACGGCATAT TTGGGAACGA 180
GAAACAAAAG TTTTCCCAA ATG AAG AGA ACT CAC TTG TTT ATT GTG GGG ATT 232
 Met Lys Arg Thr His Leu Phe Ile Val Gly Ile
 -15 -10

TAT TTT CTG TCC TCT TGC AGG GCA GAA GAG GGG CTT AAT TTC CCC ACA 280
Tyr Phe Leu Ser Ser Cys Arg Ala Glu Glu Gly Leu Asn Phe Pro Thr
 -5 1 5

TAT GAT GGG AAG GAC CGA GTG GTA AGT CTT TCC GAG AAG AAC TTC AAG 328
Tyr Asp Gly Lys Asp Arg Val Val Ser Leu Ser Glu Lys Asn Phe Lys
 10 15 20

CAG GTT TTA 337
Gln Val Leu
 25

```

## (2) INFORMATION FOR SEQ ID NO: 256:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 98..223
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 57..182  
id AA019348  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 215..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 173..287  
id AA019348  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 43..98

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..56  
id AA019348  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 98..217  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 57..176  
id AA013099  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 211..329  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 171..289  
id AA013099  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 43..98  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..56  
id AA013099  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 215..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 130..234  
id R54717  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 142..223  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 58..139  
id R54717  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 95..149  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 10..64  
id R54717  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 105..173  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..69  
id AA112675  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 215..267  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 108..160  
id AA112675  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 296..329  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 185..218  
id AA112675  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 167..196  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 62..91  
id AA112675  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 88..223  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 3..138  
id H27167  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 215..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 129..233  
id H27167  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 145..213  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.4  
seq VLLLAALPPVLLP/GA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

```

AGAGTGTTTCG CCGCCGCCGC GGCCGCCACC TGGAGTTTCT TCAGACTCCA GATTTCCTG 60
TCAACCACGA GGAGTCCAGA GAGGAAACGC GGAGGAGACA ACAGTACCTG ACGCCTCTTT 120
CAGCCCCGGA TCGCCCCAGC AGGG ATG GGC GAC AAG ATC TGG CTG CCC TTC 171
 Met Gly Asp Lys Ile Trp Leu Pro Phe
 -20 -15

CCC GTG CTC CTT CTG GCC GCT CTG CCT CCG GTG CTG CTG CCT GGG GCG 219
Pro Val Leu Leu Leu Ala Ala Leu Pro Pro Val Leu Leu Pro Gly Ala
 -10 -5 1

GCC GGC TTC ACA CCT TCC CTC GAT AGC GAC TTC ACC TTT ACC CTT CCC 267
Ala Gly Phe Thr Pro Ser Leu Asp Ser Asp Phe Thr Phe Thr Leu Pro
 5 10 15

GCC GGC CAG AAG GAG TGC TTC TAC CAG CCC ATG CCC CTG RAG GCC TCG 315
Ala Gly Gln Lys Glu Cys Phe Tyr Gln Pro Met Pro Leu Xaa Ala Ser
 20 25 30

CTG GAG ATC GAG
Leu Glu Ile Glu
35

```

## (2) INFORMATION FOR SEQ ID NO: 257:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 166..415
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..250  
id HSU52870  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 182..337
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 156..311  
id T35951  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..132
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 7..107  
id T35951  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 136..193
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 109..166  
id T35951  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 182..328
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 156..302  
id T35949  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..132
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 7..107  
id T35949  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 136..193
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 109..166  
id T35949  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 233..409
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 53..229  
id W17267  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 401..476
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 220..295  
id W17267

est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 182..399  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 54..271  
                           id HSC34G011  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 136..192  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 7..63  
                           id HSC34G011  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 306..416  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.3  
                           seq LLSACLVTWGLG/EP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

```

AATTCATTTT TCACTCCTCC CTCCTAGGTC AACTTTTCA GAAAAAGAAT CTGCATCCTG 60
GAAACCAGAA GAAAAATATG AGACGGGGAA TCATCGTGTG ATGTGTGTGC TGCCTTTGGC 120
TKWGTGTGTK GAAGTYCKG CTCAGGTGTT AGGTACAGTG TGTTTGATCG TGGTGGCTTG 180
AGGGGAACCC GCTGTTTCTG GCTGTGACTG CGGCTGCACT CAGAGAAGCT GCCCTTGGCT 240
GCTCGTAGCG CCGGGCCTTC TCTCCTCGTC ATCATCCAGA GCAGCCAGTG TCCGGGAGGC 300
ADVNG ATG CCC CAC TCC AGC CTG CAT CCA TCC ATC CCG TGT CCC AGG GGT 350
 Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly
 -35 -30 -25

CAC GGG GCC CAG AAG GCA GCC TTG GTT CTG CTG AGT GCC TGC CTG GTG 398
His Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val
 -20 -15 -10

ACC CTT TGG GGG CTA GGA GAG CCA CCA GAG CAC ACT CTC CGG TAC CTG 446
Thr Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu
 -5 1 5 10

GTG CTC CAM CTA GCC TCC CTG CAG CTG GGA 476
Val Leu Xaa Leu Ala Ser Leu Gln Leu Gly
 15 20

```

## (2) INFORMATION FOR SEQ ID NO: 258:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(28..221)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 32..225  
id AA025879  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..154)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 97..250  
id N33067  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(144..221)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 31..108  
id N33067  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..221)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 31..251  
id AA132495  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..221)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 31..251  
id AA063545  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(28..221)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98



region 47..240  
id N99132  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 59..145  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.3  
seq HLLLLLLPAPTLK/GL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ACACTCGGGC CCCACTCAAG GATGTAGGGC CTTTCTGGC CCCTGACCCC TCCCTGGC  | 58  |
| ATG GGA GCG TGG GGA CGG GGC TGG CCT TGG GAG GAG CGG CAG GGG CAT | 106 |
| Met Gly Ala Trp Gly Arg Gly Trp Pro Trp Glu Glu Arg Gln Gly His |     |
| -25 -20 -15                                                     |     |
| CAC CTC CTT CTG CTG CTT CTC CCT GCT CCT ACC CTC AAG GGC CTG GGG | 154 |
| His Leu Leu Leu Leu Leu Leu Pro Ala Pro Thr Leu Lys Gly Leu Gly |     |
| -10 -5 1                                                        |     |
| GCT GCC CAG CTG CCT CTA TGC CCT TCT GGG GGT CTC AGC CCA CTG CTG | 202 |
| Ala Ala Gln Leu Pro Leu Cys Pro Ser Gly Gly Leu Ser Pro Leu Leu |     |
| 5 10 15                                                         |     |
| ACA CTT CTG CAA TCC GGG                                         | 220 |
| Thr Leu Leu Gln Ser Gly                                         |     |
| 20 25                                                           |     |

## (2) INFORMATION FOR SEQ ID NO: 259:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 428 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 56..429  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 65..438  
id W27019  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(79..429)

(C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                           region 91..441  
                           id W26783  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 284..390  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 343..449  
                           id W85233  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 57..281  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.2  
                           seq LLFIIGLIGCCAT/IR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACTCTCGGTG AGCGCRSCCC GCTCTCCGGG CCGGGTCTTC GCGGGCCACC GGCGCC ATG | 59  |
| Met                                                               |     |
| -75                                                               |     |
| GGC CAG TGC GGC ATC ACC TCC TCC AAG ACC GTG CTG GTC TTT CTC AAC   | 107 |
| Gly Gln Cys Gly Ile Thr Ser Ser Lys Thr Val Leu Val Phe Leu Asn   |     |
| -70 -65 -60                                                       |     |
| CTC ATC TTC TGG GGG GCA GCT GGC ATT TTA TGC TAT GTG GGA GCC TAT   | 155 |
| Leu Ile Phe Trp Gly Ala Ala Gly Ile Leu Cys Tyr Val Gly Ala Tyr   |     |
| -55 -50 -45                                                       |     |
| GTC TTC ATC ACT TAT GAT GAC TAT GAC CAC TTC TTT GAA GAT GTG TAC   | 203 |
| Val Phe Ile Thr Tyr Asp Asp Tyr Asp His Phe Phe Glu Asp Val Tyr   |     |
| -40 -35 -30                                                       |     |
| ACG CTC ATC CCT GCT GTA GTG ATC ATA GCT GTA AGA GCC CTG CTT TTC   | 251 |
| Thr Leu Ile Pro Ala Val Val Ile Ile Ala Val Arg Ala Leu Leu Phe   |     |
| -25 -20 -15                                                       |     |
| ATC ATT GGG CTA ATT GGC TGC TGT GCC ACA ATC CGG GAA AGT CGC TGT   | 299 |
| Ile Ile Gly Leu Ile Gly Cys Cys Ala Thr Ile Arg Glu Ser Arg Cys   |     |
| -10 -5 1 5                                                        |     |
| GGA CTT GCC ACG TTT GTC ATC ATC CTG CTC TTG GTT TTT GTC ACA GAA   | 347 |
| Gly Leu Ala Thr Phe Val Ile Ile Leu Leu Leu Val Phe Val Thr Glu   |     |
| 10 15 20                                                          |     |
| GTT GTT GTA GTG GTT TTG GGA TAT GTT TAC AGA GCA AAG GTG GAA AAT   | 395 |
| Val Val Val Val Val Leu Gly Tyr Val Tyr Arg Ala Lys Val Glu Asn   |     |
| 25 30 35                                                          |     |
| GAG GTT GAT CGC AGC ATT CAG AAA GTG TAT AAG                       | 428 |
| Glu Val Asp Arg Ser Ile Gln Lys Val Tyr Lys                       |     |
| 40 45                                                             |     |

## (2) INFORMATION FOR SEQ ID NO: 260:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 167..425
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 106..364  
id N39913  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..170
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..108  
id N39913  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..188
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 39..166  
id HUM527C01B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 188..303
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 165..280  
id HUM527C01B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..61
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..38  
id HUM527C01B  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 81..275
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq IGHFLCLVILVYC/AE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

```

AAGAGGATTT GCGCCCTCC TCTGTGGATT CTGGCCAGGC CGGGTTCGGC GGTGCTGTG 60
AGAGCGGGCT TCCCAACACC ATG CCG KCC GCC TTC TCT GTC AGC TCT TTC CCC 113
 Met Pro Xaa Ala Phe Ser Val Ser Ser Phe Pro
 -65 -60 -55

GTC AGC ATC CCA GCC GTG CTC ACG CAG ACG GAC TGG ACT GAG CCC TGG 161
Val Ser Ile Pro Ala Val Leu Thr Gln Thr Asp Trp Thr Glu Pro Trp
 -50 -45 -40

CTC ATG GGG CTG GCC ACC TTC CAC GCG CTC TGC GTG CTC CTC ACC TGC 209
Leu Met Gly Leu Ala Thr Phe His Ala Leu Cys Val Leu Leu Thr Cys
 -35 -30 -25

TTG TCC TCC CGA AGC TAC AGA CTA CAG ATC GGG CAC TTT CTG TGT CTA 257
Leu Ser Ser Arg Ser Tyr Arg Leu Gln Ile Gly His Phe Leu Cys Leu
 -20 -15 -10

GTC ATC TTA GTC TAC TGT GCT GAA TAC ATC AAT GAG GCG GCT GCG ATG 305
Val Ile Leu Val Tyr Cys Ala Glu Tyr Ile Asn Glu Ala Ala Ala Met
 -5 1 5 10

AAC TGG AGA TTA TTT TCG MAA TAC CAG TAT TTC GAC TCC AGG GGG ATG 353
Asn Trp Arg Leu Phe Ser Xaa Tyr Gln Tyr Phe Asp Ser Arg Gly Met
 15 20 25

TTC ATT TCT ATA GTA TTT TCA GCC CCA CTG CTG GTG AAT GCC ATG ATC 401
Phe Ile Ser Ile Val Phe Ser Ala Pro Leu Leu Val Asn Ala Met Ile
 30 35 40

ATT GTG GTT ATG TGG GTA TGG AAG 425
Ile Val Val Met Trp Val Trp Lys
 45 50

```

## (2) INFORMATION FOR SEQ ID NO: 261:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 133..165  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 11..43  
id HUM153A05B  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 136..177  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.7  
seq LLLSLFFPLRISL/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

```
ATTTTCTCC GGTACAGCCT GGAACGTAG GTCCGCGCC TGTGATAAGT AAGGTTGGAT 60
TTTCTCTTCC CTGAGGTGAA GGATGCCCGG RAGSCCTCGG CAGGACCGCG CGGAAACGGG 120
CCTTCTGCCC AAAAG ATG CTG CTT CTC TCC TTA TTC TTT CCC CTC AGA ATC 171
 Met Leu Leu Leu Ser Leu Phe Phe Pro Leu Arg Ile
 -10 -5

TCG CTG TCT CCT TCC AAC CAC CTG TGG TCG GCA TCC TCC GGG 213
Ser Leu Ser Pro Ser Asn His Leu Trp Ser Ala Ser Ser Gly
 1 5 10
```

## (2) INFORMATION FOR SEQ ID NO: 262:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 16..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..304  
id HSC26A021  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 17..174

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..158  
id W07871  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 205..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 192..306  
id W07871  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 174..203  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 159..188  
id W07871  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 169..305  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 144..280  
id T75539  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 64..172  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 41..149  
id T75539  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 175..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 161..305  
id H94774  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 24..165  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 10..151  
id H94774  
est

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 228..319  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
                           region 203..294  
                           id W89738  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 43..102  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 91  
                           region 22..81  
                           id W89738  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 82..150  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.6  
                           seq LILVLQLLLRIRR/NR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

```

ACTCGCACCC GGAACAACAA AGCAAGGAAG ACGGAGTCCG AGCCTCGGGG GCTCCTAGCA 60
ACGGGCCCGGG GCGGGAGTTC C ATG GAG ACT GGG GAG CGC GCC CGT CTC ATC 111
 Met Glu Thr Gly Glu Arg Ala Arg Leu Ile
 -20 -15

CTC ATC CTT GTC CTC CAG CTT CTC CTT CGC ATC CGA CGC AAC CGG CAG 159
Leu Ile Leu Val Leu Gln Leu Leu Leu Arg Ile Arg Arg Asn Arg Gln
 -10 -5 1

CAG CGC TGC SCC GCG TCC TCA GCC ACC GCT CCC TCT TCC CAC GGA TGT 207
Gln Arg Cys Xaa Ala Ser Ser Ala Thr Ala Pro Ser Ser His Gly Cys
 5 10 15

GAT CTT CGT GGT GGA AAG CTA AAT TTT AAA ACC ACC CCA ATG GAT GCA 255
Asp Leu Arg Gly Gly Lys Leu Asn Phe Lys Thr Thr Pro Met Asp Ala
 20 25 30 35

GAC AGT GAT GTT GCA TTG GAC ATT CTA ATT ACA AAT GTA GTC TGT GTT 303
Asp Ser Asp Val Ala Leu Asp Ile Leu Ile Thr Asn Val Val Cys Val
 40 45 50

TTT AGA ACA AGA TGT CGG
Phe Arg Thr Arg Cys Arg
 55

```

## (2) INFORMATION FOR SEQ ID NO: 263:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 2..88  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 18..104  
id R56970  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 128..250  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.4  
seq ILGCSSVCQLCTG/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

```

AGGAGTTAAG AAATGTCGTT CTTCAGATTT AAAAAGAAAA CCTTTACTGA ATCAGCTGAG 60
TGTTAATAAT ACGAATTTCC TTKTCNTGCC AATKCDRMYC TGRDDCAGRA RATCSNWGAA 120
CAGGGWT ATG TGT GGA TTW YAG TTT TCT CTG CCT TGC CTA CGA CTG TTT 169
 Met Cys Gly Xaa Xaa Phe Ser Leu Pro Cys Leu Arg Leu Phe
 -40 -35 -30
CTG GTT GTT ACC TGT TAT CKT TTA TTA TTA CTC CAC AAA GAA ATA CTT 217
Leu Val Val Thr Cys Tyr Xaa Leu Leu Leu Leu His Lys Glu Ile Leu
 -25 -20 -15
GGA TGT TCG TCT GTT TGT CAG CTC TGC ACT GGG AGA CAA ATT AAC TGC 265
Gly Cys Ser Ser Val Cys Gln Leu Cys Thr Gly Arg Gln Ile Asn Cys
 -10 -5 1 5
CGT AAC TTA GGC CTT TCG AGT ATT CTA AGA ATT TTC CTG AAA GTA CAG 313
Arg Asn Leu Gly Leu Ser Ser Ile Leu Arg Ile Phe Leu Lys Val Gln
 10 15 20
TTT TTC TGT ATC
Phe Phe Cys Ile
 25

```

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 366 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR



(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 176..352  
id W42809  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..129
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 50..165  
id W42809  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..242
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 116..218  
id N99674  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 58..129
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 34..105  
id N99674  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 243..285
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 218..260  
id N99674  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..57
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 2..32  
id N99674  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..272
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 78..210  
id R20073  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 267..364
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 206..303  
id R20073  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..129
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..67  
id R20073  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..105  
id N99685  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..242
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 105..207  
id N99685  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 286..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 251..281  
id N99685  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 6..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..134

id AA154228  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 140..206  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 134..200  
id AA154228  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 10..228  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.4  
seq ACCFLSAFSPTLT/KS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ATAATAAAA ATG AAC CCC GTT ACA GAG TCA CCA TCA TGT CTC TTC TCA CCA | 51  |
| Met Asn Pro Val Thr Glu Ser Pro Ser Cys Leu Phe Ser Pro           |     |
| -70 -65 -60                                                       |     |
| CCC TCT GAA TCT GCA TTA GCC AGT CAA CTA GCC CTT TCA GCG TCA TGT   | 99  |
| Pro Ser Glu Ser Ala Leu Ala Ser Gln Leu Ala Leu Ser Ala Ser Cys   |     |
| -55 -50 -45                                                       |     |
| GAC CAG CGC GCC CCA TTC AGC TTG GCT GGT GTC GKT TCA MMA KRA CCC   | 147 |
| Asp Gln Arg Ala Pro Phe Ser Leu Ala Gly Val Xaa Ser Xaa Xaa Pro   |     |
| -40 -35 -30                                                       |     |
| AGG CTG GCC AGT CGT CAG GTT GCA CCG CCC TTT GGT TCC CGA GCA TGC   | 195 |
| Arg Leu Ala Ser Arg Gln Val Ala Pro Pro Phe Gly Ser Arg Ala Cys   |     |
| -25 -20 -15                                                       |     |
| TGT TTT CTC TCA GCC TTC TCT CCA ACC TTA ACC AAA TCG GCA GCA GCC   | 243 |
| Cys Phe Leu Ser Ala Phe Ser Pro Thr Leu Thr Lys Ser Ala Ala Ala   |     |
| -10 -5 1 5                                                        |     |
| ACC TCG ACC GCC CAC ACA TTC CTG GCC AAT CAG CTC AGC TGT TTA TTT   | 291 |
| Thr Ser Thr Ala His Thr Phe Leu Ala Asn Gln Leu Ser Cys Leu Phe   |     |
| 10 15 20                                                          |     |
| ACC AAA TGT CTT CAC AAC AAC TAC AGC AGC AGC CTT CGG CTA ACA AAA   | 339 |
| Thr Lys Cys Leu His Asn Asn Tyr Ser Ser Ser Leu Arg Leu Thr Lys   |     |
| 25 30 35                                                          |     |
| AAG CAG GAA AAA TCC ACA ACA CCC CAG                               | 366 |
| Lys Gln Glu Lys Ser Thr Thr Pro Gln                               |     |
| 40 45                                                             |     |

## (2) INFORMATION FOR SEQ ID NO: 265:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 base pairs  
(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 2..86  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 8..92  
id AA070287  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 15..80  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..66  
id T10748  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 22..88  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 17..83  
id N67981  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 21..85  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 17..81  
id AA069568  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 25..87  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.3  
seq LGLSVLLTAATVA/GV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

AAGGCCGCGG CCGCCAGCGT GGGG ATG TCT AGG AGC TCG AAG GTG GTG CTG 51  
Met Ser Arg Ser Ser Lys Val Val Leu  
-20 -15

GGC CTC TCG GTG CTG CTG ACG GCG GCC ACA GTG GCC GGC GTA CAT GTG 99  
Gly Leu Ser Val Leu Leu Thr Ala Ala Thr Val Ala Gly Val His Val

-10

-5

1

AAG CAG CAG TGG GAC  
Lys Gln Gln Trp Asp  
5

114

## (2) INFORMATION FOR SEQ ID NO: 266:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..197
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 8..204  
id H10448  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..197
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..193  
id AA127134  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..197
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..193  
id HUML13653  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..197
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 9..205  
id HSC18H071  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 34..197

(C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                             region 13..176  
                             id AA194682  
                             est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 31..108  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.3  
                             seq GVGLVTLLGLAVG/SY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| GTCAGGTGGT GGAGGAAAAG GCGCTCCGTC ATG GGG ATC CAG ACG AGC CCC GTC | 54  |
| Met Gly Ile Gln Thr Ser Pro Val                                  |     |
| -25 -20                                                          |     |
| CTG CTG GCC TCC CTG GGG GTG GGG CTG GTC ACT CTG CTC GGC CTG GCT  | 102 |
| Leu Leu Ala Ser Leu Gly Val Gly Leu Val Thr Leu Leu Gly Leu Ala  |     |
| -15 -10 -5                                                       |     |
| GTG GGC TCC TAC TTG GTT CGG AGG TCC CGC CGG CCT CAG GTC ACT CTC  | 150 |
| Val Gly Ser Tyr Leu Val Arg Arg Ser Arg Arg Pro Gln Val Thr Leu  |     |
| 1 5 10                                                           |     |
| CTG GAC CCC AGT GAA AAG TAC CTG CTA CGA CTG CTA GAC AAG ACG ACC  | 198 |
| Leu Asp Pro Ser Glu Lys Tyr Leu Leu Arg Leu Leu Asp Lys Thr Thr  |     |
| 15 20 25 30                                                      |     |
| CCC GGG                                                          | 204 |
| Pro Gly                                                          |     |

## (2) INFORMATION FOR SEQ ID NO: 267:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 33..227  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                             region 1..195  
                             id W00881  
                             est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 167..319  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.2  
 seq VLLSSAXLVXXS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

```

CATTGCTCT TCTCTTAACT CCTACCTGAA AACCCCATTC CTAAATTATT CACTATATTT 60
CAGACTTCTT CACTCTTCTC CMAAAACCTG AATCAGCTTG TGCTGATTTT TTCCTATCTG 120
CTATCCCTAA AAGGACTAGA CCTTCTTTCT ATCCTTACTC CCCTCA ATG TAT CCA 175
 Met Tyr Pro
 -50

TCT TAC CTC TTG ATT KKS CCT CCC ATT CCC TCA CAG TTC CTG AAA CAG 223
Ser Tyr Leu Leu Ile Xaa Pro Pro Ile Pro Ser Gln Phe Leu Lys Gln
 -45 -40 -35

TGC SCC CCC CCG ACC CTA AGC GAC CCC TTT CTG CCC CTG GCC TTG AGG 271
Cys Xaa Pro Pro Thr Leu Ser Asp Pro Phe Leu Pro Leu Ala Leu Arg
 -30 -25 -20

TCC CTT GAC GTG CTG CTC CTG TCT TCT GCT CNB YTA GTB VVC NAT TCC 319
Ser Leu Asp Val Leu Leu Leu Ser Ser Ala Xaa Leu Val Xaa Xaa Ser
 -15 -10 -5

TCT CCC TTG GAA TTC ATC AGA 340
Ser Pro Leu Glu Phe Ile Arg
 1 5

```

(2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 368 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 253..332  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 90  
 region 159..238  
 id AA114672  
 est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

- (B) LOCATION: 195..293  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.2  
 seq ILLXTFQTWCLR/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

```

AGGGGTACCT GGTCGTCATG GCAGGCGGTA TTGACCGAAG AGCTTGRTGA GGAAGAGCAG 60
CTGCTGAGAA GGCATCGCAA AKAGAAGAAG GAGTTGCAAS CCAAAATTCA GGGCATGAAG 120
AATGCTGTTC CCAAGAATGA CAATGAAGAG GDAGGARGCA GCTCACCGRG GATGTGGCCA 180
AGTTGGAAAA AGAW ATG GAA CAG AAA CAY AGA GAS GAA CTG GAG CAA TTG 230
 Met Glu Gln Lys His Arg Xaa Glu Leu Glu Gln Leu
 -30 -25

AAG CTG RCT ACT AAG GAG AAT AAG ATT CTG TTG CTG YWA ACA TTT CAA 278
Lys Leu Xaa Thr Lys Glu Asn Lys Ile Leu Leu Leu Xaa Thr Phe Gln
 -20 -15 -10

ACT TGG TGC TTG AGA ATC AGC CAC CTC GGA TAT CAR AAG CAC AWA AGA 326
Thr Trp Cys Leu Arg Ile Ser His Leu Gly Tyr Gln Lys His Xaa Arg
 -5 1 5 10

GRC GGG TGC CTG GAT MSA AGG AGC TCT CTG TGT TGT CCT TGG 368
Xaa Gly Cys Leu Asp Xaa Arg Ser Ser Leu Cys Cys Pro Trp
 15 20 25

```

(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other  
 (B) LOCATION: complement(1..43)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 90  
 region 209..251  
 id AA013573  
 est

(ix) FEATURE:

- (A) NAME/KEY: other  
 (B) LOCATION: complement(1..43)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 90



region 153..195  
id AA014924  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 54..122  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.9  
seq TLKFLTLQKSNA/KR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

```

AGACGAAGCT CGATGAAGAT TTAGAGAGTT CCAGTGAATC CGATGTGAGT CTG ATG 56
 Met

ATG ACA GCA CCT GTT CTA GCA GCT CAG ACT CTG AAG TTT TTG ACG TTA 104
Met Thr Ala Pro Val Leu Ala Ala Gln Thr Leu Lys Phe Leu Thr Leu
 -20 -15 -10

TTG CAG AAA TCA AAC GCA AAA AGG SCC AAC CTT GAC CGA CTT CAT GAT 152
Leu Gln Lys Ser Asn Ala Lys Arg Xaa Asn Leu Asp Arg Leu His Asp
 -5 1 5 10

GAA CTT TGG TAC AAC GAT CCA GGC CAG ATG AAT GAT GGA CCA CTC TGC 200
Glu Leu Trp Tyr Asn Asp Pro Gly Gln Met Asn Asp Gly Pro Leu Cys
 15 20 25

AAA TGC AGC GCA AAG GCA AGA CGC ACA GGA ATT AGG CAC AGC ATT TAT 248
Lys Cys Ser Ala Lys Ala Arg Arg Thr Gly Ile Arg His Ser Ile Tyr
 30 35 40

CCT GGA GAA GAG GCC ATC AAG CCC TGT CGT CCT ATG ACC AAC AAT GCT 296
Pro Gly Glu Glu Ala Ile Lys Pro Cys Arg Pro Met Thr Asn Asn Ala
 45 50 55

GGC AGA CTT TTC CAC TAC CGG ATC ACA GTM TCC CCG CCT ACG AAC TTT 344
Gly Arg Leu Phe His Tyr Arg Ile Thr Val Ser Pro Pro Thr Asn Phe
 60 65 70

TTA ACT GAC AGG CCA ACT GTT ATA GAA TAC GAT GAT CAC GAG TAT ATC 392
Leu Thr Asp Arg Pro Thr Val Ile Glu Tyr Asp Asp His Glu Tyr Ile
 75 80 85 90

TTT GAA
Phe Glu
 398

```

## (2) INFORMATION FOR SEQ ID NO: 270:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 359 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 105..208  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 81..184  
                           id N51797  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 30..110  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 7..87  
                           id N51797  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 54..134  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.9  
                           seq ALALAXAPDLAQA/PL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

```

AGTGCAGAAG GTTCTGGGAA GTAGGAGACC CCACTGGCTT TGGTCCCCTA AGA ATG 56
 Met

GAC TCT GCT GCC TGT GCT GCT GCT GCC ACC CCT GTT CCA GCC CTG GCT 104
Asp Ser Ala Ala Cys Ala Ala Ala Ala Thr Pro Val Pro Ala Leu Ala
-25 -20 -15

TTG GCC HTA GCT CCA GAC CTA GCA CAA GCC CCA CTG GCA CTC CCT GGC 152
Leu Ala Xaa Ala Pro Asp Leu Ala Gln Ala Pro Leu Ala Leu Pro Gly
-10 -5 1 5

CTG TTA AGC CCA TCT TGC CTT CTC TCC TCT GGA CAA GAA GTA AAT GGG 200
Leu Leu Ser Pro Ser Cys Leu Leu Ser Ser Gly Gln Glu Val Asn Gly
10 15 20

AGT GAA AGA GGA ACT TGT CTC TGG AGG CCC TGG CTG TCT TCC ACA AAT 248
Ser Glu Arg Gly Thr Cys Leu Trp Arg Pro Trp Leu Ser Ser Thr Asn
25 30 35

GAC TCC CCA AGG CAG ATG AGG AAG CTG GTG GAT TTG GCT GCT GGT GGG 296
Asp Ser Pro Arg Gln Met Arg Lys Leu Val Asp Leu Ala Ala Gly Gly
40 45 50

GCA ACG GCT GCT GAG GTC ACC AAG GCT GAA TCC ATR NTC CAT CAC CCT 344
Ala Thr Ala Ala Glu Val Thr Lys Ala Glu Ser Xaa Xaa His His Pro
55 60 65 70

GTC AGG CTC TTC TGG
Val Arg Leu Phe Trp
359

```

## (2) INFORMATION FOR SEQ ID NO: 271:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..304
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 15..317  
id T86266  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 64..135
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq ILGLLGLLGTLVA/ML

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

```

AAAGAGCTTC AGCCTGAAGA CAAGGGAGCA GTCCCTGAAG ACGCTTCTAC TGAGAGGTCT 60
GCC ATG GCC TCT CTT GGC CTC CAA CTT GTG GGC TAC ATC CTA GGC CTT 108
 Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu
 -20 -15 -10

CTG GGG CTT TTG GGS ACA CTG GTT GCC ATG CTG CTC CCC AGC TGG AAA 156
Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp Lys
 -5 1 5

ACA AGT TCT TAT GTC GGT GCC AGC ATT GTG ACA GCA GTT GGC TTC TCC 204
Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly Phe Ser
 10 15 20

AAG GGC CTC TGG ATG GAA TGT GCC ACA YAC AGC ACA GGC ATC ACC CAG 252
Lys Gly Leu Trp Met Glu Cys Ala Thr Xaa Ser Thr Gly Ile Thr Gln
 25 30 35

TGT GAC ATC TAT AGC ACC CTT CTG GGC CTG CCC GCT GAC ATC CAG GCT 300
Cys Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala Asp Ile Gln Ala
 40 45 50 55

GCC CAG GCC ATG ATG GTG ACA TCC AGT GCA ATC TCC TCC CTG GCC TGC 348

```

```

Ala Gln Ala Met Met Val Thr Ser Ser Ala Ile Ser Ser Leu Ala Cys
 60 65 70

ATT ATC TCT GTG GTG GGC ATG AGA TGC ACA GTC TTC TGC CAG GAA TCC 396
Ile Ile Ser Val Val Gly Met Arg Cys Thr Val Phe Cys Gln Glu Ser
 75 80 85

CGA GCC AGG
Arg Ala Arg
 90

```

## (2) INFORMATION FOR SEQ ID NO: 272:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 98..326
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 15..243  
id T86266  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 160..231
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq ILGLLGLLGTLVA/ML

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

```

AGCTGCTTGT GGCCACCCAC AGACACTTGT AAGGAGGAGA GAAGTCAGCC TGGCAGAGAG 60
ACTCTGAAAT GASSGATTAG AGGTGTTCAA GGRAGCAAAG AGCTTCAGCC TGAAGACAAG 120
GGAGCAGTCC CTGAAGACGC TTCTACTGAG AGGTCTGCC ATG GCC TCT CTT GGC 174
 Met Ala Ser Leu Gly
 -20
CTC CAA CTT GTG GGC TAC ATC CTA GGC CTT CTG GGG CTT TTG GGC ACA 222
Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu Gly Leu Leu Gly Thr
 -15 -10 -5
CTG GTT GCC ATG CTG CTC CCC AGC TGG AAA ACA AGT TCT TAT GTC GGT 270
Leu Val Ala Met Leu Leu Pro Ser Trp Lys Thr Ser Ser Tyr Val Gly

```

1

5

10

GCC AGC ATT GTG ACA GCA GTT GGC TTC TCC AAG GGC CTC TGG ATG GAA 318  
 Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys Gly Leu Trp Met Glu  
           15                                  20                                  25

TGT GCC  
 Cys Ala 324  
           30

(2) INFORMATION FOR SEQ ID NO: 273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 95..260
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
                                   region 19..184  
                                   id AA132585  
                                   est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 347..399
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
                                   region 2..54  
                                   id N57441  
                                   est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 272..325
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
                                   seq LLCECLLLVAGYA/HD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

ACGCAGCCGT CAGCCGAACA ATTCGATGAC GAGGCCCAGG AAGCACGCTG AAACCCTGGG 60  
 CGGCGGCAAG CTGTGCGACC TCTTCTGCGG CCGGCCTGGA CTAGCTTTAT CGTCATCTGG 120  
 GAAATGTGTTA AAAATGCAAA TTCGCAAGTT TGAGAGCCAT GGTTC CAAGA AACTGCATAA 180

```

GCATACGAAA TAAGTTGCAG CCTCCCGWCT TATACCCTGG TACTTCTAGT CTAAAACAGG 240
ATTGACTCT ACTAATCCAG CCTTATACAG G.ATG CTG TGT TCT TTG CTC CTT 292
 Met Leu Cys Ser Leu Leu Leu
 -15

TGT GAA TGT CTG TTG CTG GTA GCT GGT TAT GCT CAT GAT GAT GAC TGG 340
Cys Glu Cys Leu Leu Leu Val Ala Gly Tyr Ala His Asp Asp Asp Trp
 -10 -5 1 5

ATT GAC CCC ACA GAC ATG CTT AAC TAT GAT GCT GCT TCA GGA ACA ATG 388
Ile Asp Pro Thr Asp Met Leu Asn Tyr Asp Ala Ala Ser Gly Thr Met
 10 15 20

AGA AAA TCT 397
Arg Lys Ser

```

## (2) INFORMATION FOR SEQ ID NO: 274:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..42
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 14..55  
id H32593  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 22..87
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq LWYVCPCPSGAWM/VP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

```

AGACGCTGCC CTTCCGCAGC G ATG GCA TCC CGG CTC TGT GGA GGG GCC CTC 51
 Met Ala Ser Arg Leu Cys Gly Gly Ala Leu
 -20 -15

TGG TAT GTG TGT CCC TGT CCT TCT GGG GCG TGG ATG GTK CCT GGG 96
Trp Tyr Val Cys Pro Cys Pro Ser Gly Ala Trp Met Val Pro Gly
 -10 -5 1

```

## (2) INFORMATION FOR SEQ ID NO: 275:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..254
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 15..250  
id H23844  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 25..254
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 8..237  
id AA036876  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..254
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 21..251  
id H22656  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..217
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..183  
id W05714  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 218..254
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 183..219  
id W05714  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 34..244
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..211  
id AA100765  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 69..152
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq LGYLVLSEGAFLA/SS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

```

ACGTGACCGG GGCCTGAAGC CGGAAGCTAC CTATCTGGTA GGGAGCTCCC CCAGCACCGA 60
AGACTGCG ATG ACT TCT GCA CTG ACC CAG GGG CTG GAG CGA ATC CCA GAC 110
 Met Thr Ser Ala Leu Thr Gln Gly Leu Glu Arg Ile Pro Asp
 -25 -20 -15

CAG CTC GGC TAC CTG GTA CTG AGT GAA GGT GCA GTG CTG GCG TCA TCT 158
Gln Leu Gly Tyr Leu Val Leu Ser Glu Gly Ala Val Leu Ala Ser Ser
 -10 -5 1

GGG GAC CTG GAG AAT GAT GAG CAG GCA DCC AGT GCC ATC TCT GAG CTG 206
Gly Asp Leu Glu Asn Asp Glu Gln Ala Xaa Ser Ala Ile Ser Glu Leu
 5 10 15

GTC AGC ACA GCC TGC GGT TTC CGG CTG CAC CGC GGC ATG AAT GTG CCC 254
Val Ser Thr Ala Cys Gly Phe Arg Leu His Arg Gly Met Asn Val Pro
 20 25 30

AGG 257
Arg
35

```

## (2) INFORMATION FOR SEQ ID NO: 276:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 9..243



(C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 6..245  
                           id H64050  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 15..248  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 1..234  
                           id R17172  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 14..248  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
                           region 1..235  
                           id HSC15C081  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 22..248  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 1..227  
                           id AA149663  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 43..248  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
                           region 29..234  
                           id HSU46380  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 24..149  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.4  
                           seq ITGVILLAVGIWG/KV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

```

AGGTGCAGGG TCTCGGGCTA GTC ATG GCG TCC CCG TCT CGG AGA CTG CAG ACT 53
 Met Ala Ser Pro Ser Arg Arg Leu Gln Thr
 -40 -35

AAA CCA GTC ATT ACT TGT TTC AAG AGC GTT CTG CTA ATC KAC ACT NTK 101
Lys Pro Val Ile Thr Cys Phe Lys Ser Val Leu Leu Ile Xaa Thr Xaa
 -30 -25 -20

ATT TKC TGG ATC ACT GGC GTK ATC CTT CTT GCA GTT GGC ATT TGG GGC 149

```

```

Ile Xaa Trp Ile Thr Gly Val Ile Leu Leu Ala Val Gly Ile Trp Gly
-15 -10 -5

AAG GTG AGC CTG GAG AAT TAC TTT KCK CTT TTA AAT GAG AAG GCC ACC 197
Lys Val Ser Leu Glu Asn Tyr Phe Xaa Leu Leu Asn Glu Lys Ala Thr
 1 5 10 15

AAT GTC CCC TTC GKG CTC ATT GCT ACT GGT ACC GTC ATK ATT CTT TTG 245
Asn Val Pro Phe Xaa Leu Ile Ala Thr Gly Thr Val Xaa Ile Leu Leu
 20 25 30

GGC TAC CGG 254
Gly Tyr Arg
 35

```

## (2) INFORMATION FOR SEQ ID NO: 277:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..228
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 19..246  
id HUMHG1206  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..222  
id C15962  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 35..220  
id HUM417F07B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 2..33  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 1..32  
                           id HUM417F07B  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 59..228  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 18..187  
                           id AA139623  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 94..178  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 1..85  
                           id N88476  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 177..228  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
                           region 82..133  
                           id N88476  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 49..108  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.3  
                           seq VLLGSGLTILSQP/LM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GTCGCTTGGT GGCTCCGTCT GTCTGTCCGT CCGCCGCGG GTGCCATC ATG GCG GAC | 57  |
| Met Ala Asp                                                     |     |
| -20                                                             |     |
| GCG GCC AGT CAG GTG CTC CTG GGC TCC GGT CTC ACC ATC CTG TCC CAG | 105 |
| Ala Ala Ser Gln Val Leu Leu Gly Ser Gly Leu Thr Ile Leu Ser Gln |     |
| -15 -10 -5                                                      |     |
| CCG CTC ATG TAC GTG AAA GTG CTC ATC CAG GTG GGA TAT GAG CCT CTT | 153 |
| Pro Leu Met Tyr Val Lys Val Leu Ile Gln Val Gly Tyr Glu Pro Leu |     |
| 1 5 10 15                                                       |     |
| CCT CCA ACA ATA GGA CGA AAT ATT TTT GGG CGG CAA GTG TGN YAG CTT | 201 |
| Pro Pro Thr Ile Gly Arg Asn Ile Phe Gly Arg Gln Val Xaa Xaa Leu |     |
| 20 25 30                                                        |     |
| CCT NGT CTC TTT AGT TAT GCT CAG CAC GGG                         | 231 |

Pro Xaa Leu Phe Ser Tyr Ala Gln His Gly  
35 40

(2) INFORMATION FOR SEQ ID NO: 278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..185)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 93..276  
id AA136898  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 43..89
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 30..76  
id W96077  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 125..161
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 110..146  
id W96077  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 83..119
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 69..105  
id W96077  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..49
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 1..35

id W96077  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 126..161  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 129..164  
id N41630  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 58..89  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 63..94  
id N41630  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 2..31  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 7..36  
id N41630  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 38..161  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 19..142  
id AA043148  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 121..185  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 61..125  
id HUM430A04B  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 60..119  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..60  
id HUM430A04B  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 98..157  
(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.3  
seq ALIFGGFISLIGA/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

```

AACCTCTTCC GAGCGGGGTC ACGGCCCCGGC CGTCGGTAAC CTGGTTTCCG AGAGTGCCGG 60
GCGGTCGGCG GGTCAAGGCA GCCCGGGGCC TGACGCC ATG TCC CGG AAC CTG CGC 115
 Met Ser Arg Asn Leu Arg
 -20 -15

ACC GCG CTC ATT TTC GGC GGC TTC ATC TCC CTG ATC GGC GCC GCC TTC 163
Thr Ala Leu Ile Phe Gly Gly Phe Ile Ser Leu Ile Gly Ala Ala Phe
 -10 -5 1

TAT CCC ATC TAC TTC CGA CCC CAT GGG 190
Tyr Pro Ile Tyr Phe Arg Pro His Gly
 5 10

```

(2) INFORMATION FOR SEQ ID NO: 279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(97..229)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 10..142  
id H62783  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 80..218
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 54..192  
id T71240  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 148..221
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 356..429

id AA075451  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 80..140  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 288..348  
id AA075451  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 135..222  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 350..437  
id AA009954  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 105..140  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 319..354  
id AA009954  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 148..216  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 384..452  
id W15396  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 80..117  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 315..352  
id W15396  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 206..256  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.1  
seq LWCFHLVVLSLYS/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

ATGAGTGTG ATGTTTTCT GCACTAGAAG GCACTATGTT GAACTATTAA ACTTACCAGC 60  
ACTTTCTTTT TCCACTCCAT AGTTTCATTG TACTGACAAC CTCAGCTGGC ATCATGGACC 120

ATGAAGAAGC AAGACGAAAA CACACAGGRA GGGAAATCC TGGGATTCTT TTTCTAGGGA 180  
TGTAATACAT ATATTTACAA ATAAA ATG CCT CAT GGA CTC TGG TGC TTC CAC 232  
Met Pro His Gly Leu Trp Cys Phe His  
-15 -10  
TTG GTC GTT TTG AGC CTT TAC AGC AGT GTA GCC ACA GCC CGG 274  
Leu Val Val Leu Ser Leu Tyr Ser Ser Val Ala Thr Ala Arg  
-5 1 5

## (2) INFORMATION FOR SEQ ID NO: 280:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..124)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 104..226  
id W94087  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..124
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 12..134  
id R37206  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..124
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 19..141  
id N42384  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..92)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 177..267



id H84930  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(81..124)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 144..187  
id H84930  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(2..124)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 148..270  
id H82795  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 21..62  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5  
seq SLVAVFLSCGLIS/KN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ATAAATTAGC AGTATTAGTT ATG AGT TTG GTT GCA GTG TTC TTA TCT TGT GGG | 53  |
| Met Ser Leu Val Ala Val Phe Leu Ser Cys Gly                       |     |
| -10 -5                                                            |     |
| CTG ATT TCC AAA AAC CAC ATG CTG CTG AAT TTA CCA GGG ATC CTC ATA   | 101 |
| Leu Ile Ser Lys Asn His Met Leu Leu Asn Leu Pro Gly Ile Leu Ile   |     |
| 1 5 10                                                            |     |
| CCT CAC AAT GCA AAC CAC TTA CTG                                   | 125 |
| Pro His Asn Ala Asn His Leu Leu                                   |     |
| 15 20                                                             |     |

## (2) INFORMATION FOR SEQ ID NO: 281:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Kidney

## (ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 2..85  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 91  
                           region 4..87  
                           id HUML1521  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 85..120  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
                           region 86..121  
                           id HUML1521  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 89..148  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 123..182  
                           id W52706  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 34..84  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 69..119  
                           id W52706  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(75..148)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 91  
                           region 324..397  
                           id AA132959  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 27..98  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5  
                           seq GALAVGAVPVVLS/AM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

```

AAAGTTGNSA CCCGGACGGC CTCACC ATG ATG AAA CGG GCA GCT GCT GCT GCA 53
 Met Met Lys Arg Ala Ala Ala Ala Ala
 -20

GTG GGA GGA GCC CTG GCA GTG GGG GCT GTG CCC GTG GTG CTC AGT GCC 101
Val Gly Gly Ala Leu Ala Val Gly Ala Val Pro Val Val Leu Ser Ala
-15 -10 -5 1

```

ATG GGC TTC ACT GGG GCA GGA ATC GCC GCG TCC TCC ATA GCA GCC CAT 149  
 Met Gly Phe Thr Gly Ala Gly Ile Ala Ala Ser Ser Ile Ala Ala His  
                   5                                  10                                  15

GGG 152  
 Gly

## (2) INFORMATION FOR SEQ ID NO: 282:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 232..430
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
                                   region 14..212  
                                   id H14129  
                                   est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 19..261
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9  
                                   seq LISFSWFANYIRA/GT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

ATTGCCTTCA TTGCCGGC ATG GCC GTC ATT GTG GAT AAA CCC TGG TTC TAT 51  
                   Met Ala Val Ile Val Asp Lys Pro Trp Phe Tyr  
                   -80                                  -75

GAC ATG AAG AAA GTT TGG GAG GGA TAT CCC ATA CAG AGC ACT ATC CCT 99  
 Asp Met Lys Lys Val Trp Glu Gly Tyr Pro Ile Gln Ser Thr Ile Pro  
 -70                  -65                                  -60                                  -55

TCC CAG TAT TGG TAC TAC ATG ATT GAA CTT TCC TTC TAC TGG TCC CTG 147  
 Ser Gln Tyr Trp Tyr Tyr Met Ile Glu Leu Ser Phe Tyr Trp Ser Leu  
                   -50                                  -45                                  -40

CTC TTC AGC ATT GCC TCT GAT GTC AAG CGA AAG GAT TTC AAG GAA CAG 195  
 Leu Phe Ser Ile Ala Ser Asp Val Lys Arg Lys Asp Phe Lys Glu Gln  
                   -35                                  -30                                  -25

ATC ATC CAC CAT GTG GCC ACC ATC ATT CTC ATC AGC TTT TCC TGG TTT 243  
 Ile Ile His His Val Ala Thr Ile Ile Leu Ile Ser Phe Ser Trp Phe

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| -20                                                             | -15 | -10 |     |
| GCC AAT TAC ATC CGA GCT GGG ACT CTA ATC ATG GCT CTG CAT GAC TCT |     |     | 291 |
| Ala Asn Tyr Ile Arg Ala Gly Thr Leu Ile Met Ala Leu His Asp Ser |     |     |     |
| -5                                                              | 1   | 5   | 10  |
| TCC GAT TAC CTG CTG GAG TCA GCC AAG ATG TTT AAC TAC GCG GGA TGG |     |     | 339 |
| Ser Asp Tyr Leu Leu Glu Ser Ala Lys Met Phe Asn Tyr Ala Gly Trp |     |     |     |
|                                                                 | 15  | 20  | 25  |
| AAG AAC ACC TGC AAC AAC ATC TTC ACC GTC TTC GCC ATT GTT TTT ATC |     |     | 387 |
| Lys Asn Thr Cys Asn Asn Ile Phe Thr Val Phe Ala Ile Val Phe Ile |     |     |     |
|                                                                 | 30  | 35  | 40  |
| ATC ACC CGA CTG GTC ATC CTG CCC TTC TGG ATC CTG CAT TGC         |     |     | 429 |
| Ile Thr Arg Leu Val Ile Leu Pro Phe Trp Ile Leu His Cys         |     |     |     |
|                                                                 | 45  | 50  | 55  |

## (2) INFORMATION FOR SEQ ID NO: 283:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..221
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 37..147  
id T82645  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 35..82
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq SLFIYIFLTCSNT/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ATAGTATCTA TTGAAAAGGA AGCAGTGTGT ATCT ATG ATT ATA TCT CTG TTC ATC | 55  |
| Met Ile Ile Ser Leu Phe Ile                                       |     |
| -15                                                               | -10 |
| TAT ATA TTT TTG ACA TGT AGC AAC ACC TCT CCA TCT TAT CAA GGA ACT   | 103 |
| Tyr Ile Phe Leu Thr Cys Ser Asn Thr Ser Pro Ser Tyr Gln Gly Thr   |     |
| -5                                                                | 1   |
|                                                                   | 5   |

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CAA CTC GGT CTG GGT CTC CCC AGT GCC CAG TGG TGG CCT TTG ACA GGT | 151 |
| Gln Leu Gly Leu Gly Leu Pro Ser Ala Gln Trp Trp Pro Leu Thr Gly |     |
| 10 15 20                                                        |     |
| AGG AGG ATG CAG TGC TGC AGG CTA TTT TGT TTT TTG TTA CAA AAC TGT | 199 |
| Arg Arg Met Gln Cys Cys Arg Leu Phe Cys Phe Leu Leu Gln Asn Cys |     |
| 25 30 35                                                        |     |
| CTT TTC CCT TTT CCC CTC CAC CTG ATT CAG CAT GAT CCC TGT GAG CTG | 247 |
| Leu Phe Pro Phe Pro Leu His Leu Ile Gln His Asp Pro Cys Glu Leu |     |
| 40 45 50 55                                                     |     |
| GTT CTC ACA ATC TCT GGG ACT                                     | 268 |
| Val Leu Thr Ile Ser Gly Thr                                     |     |
| 60                                                              |     |

## (2) INFORMATION FOR SEQ ID NO: 284:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 9..250
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 7..248  
id HSC2OD111  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 122..257
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..136  
id T77096  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..146
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 19..147  
id N32450  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 9..104
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq LQMLLG FVGRSKS/GL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

```

AGACCAAG ATG GCG GCG GAG CTG GTG GAG GCC AAA AAC ATG GTG ATG AGT 50
 Met Ala Ala Glu Leu Val Glu Ala Lys Asn Met Val Met Ser
 -30 -25 -20

TTT CGA GTC TCC GAC CTT CAG ATG CTC CTG GGT TTC GTG GGC CGG AGT 98
Phe Arg Val Ser Asp Leu Gln Met Leu Leu Gly Phe Val Gly Arg Ser
 -15 -10 -5

AAG AGT GGA CTG AAG CAC GAG CTC GTC ACC AGG GCC CTC CAG CTG GTG 146
Lys Ser Gly Leu Lys His Glu Leu Val Thr Arg Ala Leu Gln Leu Val
 1 5 10

CAG TTT GAC TGT AGC CCT GAG CTG TTC AAG AAG ATC AAG GAG CTG TAC 194
Gln Phe Asp Cys Ser Pro Glu Leu Phe Lys Lys Ile Lys Glu Leu Tyr
 15 20 25 30

GAG ACC CGC TAC GCC AAG AAG AAC TCG GAG CCT GCC CCA CAG CCG CAC 242
Glu Thr Arg Tyr Ala Lys Lys Asn Ser Glu Pro Ala Pro Gln Pro His
 35 40 45

CGG CCC CTG GAC CCC CTG ACC GGG 266
Arg Pro Leu Asp Pro Leu Thr Gly
 50

```

## (2) INFORMATION FOR SEQ ID NO: 285:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 10..105
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 1..96  
id R05622  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 24..92  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
 region 2..70  
 id H94933  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 64..243  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.7  
 seq VHALCPLSPLVTT/GC

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

```

AACTCTCCAA AAAGCAGAGA CAGCAGGAAG AGGGGAGTGG AGGCAGCCCA TTCACCTGGG 60
GAA ATG ACT GGG TTG TCG ATG GMC GGT GGC GGB AGC CSA AMG GGG GAY 108
 Met Thr Gly Leu Ser Met Xaa Gly Gly Gly Ser Xaa Xaa Gly Asp
 -60 -55 -50

GTG GAS CCG TDC TAC TAT GGT AAR CVT GGG CCC CTG CGC RCC CTT CCT 156
Val Xaa Pro Xaa Tyr Tyr Gly Lys Xaa Gly Pro Leu Arg Xaa Leu Pro
 -45 -40 -35

GAG CCC TCA GGA CCC CTT CCA CCA AGC AGC GGC CTC TCC CAG CCC CAG 204
Glu Pro Ser Gly Pro Leu Pro Pro Ser Ser Gly Leu Ser Gln Pro Gln
 -25 -20 -15

GTC CAT GCT CTG TGC CCC TTA TCT CCC CTG GTT ACC ACG GGC TGC TGC 252
Val His Ala Leu Cys Pro Leu Ser Pro Leu Val Thr Thr Gly Cys Cys
 -10 -5 1

GGG CAG GCT GCG
Gly Gln Ala Ala
 5

```

## (2) INFORMATION FOR SEQ ID NO: 286:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 157..269  
 (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97  
region 95..207  
id N41379  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 62..173  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 1..112  
id N41379  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 275..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 213..257  
id N41379  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 8..173  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 1..166  
id AA044371  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 157..219  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 149..211  
id AA044371  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(272..319)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 423..470  
id N30852  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(225..264)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 478..517  
id N30852  
est

(ix) FEATURE:

(A) NAME/KEY: other



(B) LOCATION: complement(320..349)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 394..423  
                           id N30852  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(238..271)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
                           region 481..514  
                           id AA044232  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 303..349  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 5..51  
                           id R78468  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 367..459  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.6  
                           seq GLLGXGLXXXSLT/AG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

```

AAAGTCCTAG AGGGGGTCGG GGTMTGGGTG GACAAGCTTT CCTCGTCCTC TCCCNACAGA 60
GCTGACGTGT CCTGGGTTC ACCGGGAGCG GGCATTTC CA CCGGACGGGA GGGTTCGGGG 120
TGTCCGGGGC TGGGGAATAC GTARGGGKTG CSGCGCCGGT GTGGGAAGTT GGGGCGTGTG 180
GCTGCAGTCC CGGGAGTTCT TGGAGGGGGT CGGCCACCG AGCTTCCGGA CCGGCTGATC 240
TGCCCGTAGC TTGCCGGAGG GAGGGCGGAG CTGACTCTCC GTCCCTTCTC CCATCCCCTC 300
SAGTGGTGGG TACGGGCACC TCGCTGGCGC TCTCCTCCCT CCTGTCCCTN GNNSNTCTTT 360
GCTGGG ATG CAG ATG TAC AGC CGT CAG CTG GCC TCC AMC GAG TGG CTC 408
 Met Gln Met Tyr Ser Arg Gln Leu Ala Ser Xaa Glu Trp Leu
 -30 -25 -20

ACC ATC CAG GGC GGC CTG CTT GGW KCG GGT CTC TTS KRG TYC TCG CTC 456
Thr Ile Gln Gly Gly Leu Leu Gly Xaa Gly Leu Xaa Xaa Xaa Ser Leu
 -15 -10 -5

ACT GCG GGG
Thr Ala Gly
1

```

## (2) INFORMATION FOR SEQ ID NO: 287:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..344
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 56..337  
id AA203498  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 7..65
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..59  
id AA203498  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 344..385
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 338..379  
id AA203498  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..292
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 44..273  
id W87295  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 292..344
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 274..326  
id W87295  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 20..65  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 2..47  
id W87295  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 344..385  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 327..368  
id W87295  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 33..344  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..312  
id AA248429  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 344..385  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 313..354  
id AA248429  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 76..344  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..269  
id W01758  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 344..385  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 270..311  
id W01758  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 63..234  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 30..201  
id AA249697  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 33..65  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 1..33  
                           id AA249697  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 257..289  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 222..254  
                           id AA249697  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 227..256  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 193..222  
                           id AA249697  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 19..180  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.3  
                           seq LIVWLLVKSFSES/GI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATCTGGCTCA GTTCCGCC ATG GCC TCC TTG GAA GTC AGT CGT AGT CCT CGC | 51  |
| Met Ala Ser Leu Glu Val Ser Arg Ser Pro Arg                     |     |
| -50 -45                                                         |     |
| AGG TCT CGG CGG GAG CTG GAA GTG CGC AGT CCA CGA CAG AAC AAA TAT | 99  |
| Arg Ser Arg Arg Glu Leu Glu Val Arg Ser Pro Arg Gln Asn Lys Tyr |     |
| -40 -35 -30                                                     |     |
| TCG GTG CTT TTA CCT ACC TAC AAC GAG CGC GAG AAC CTG CCG CTC ATC | 147 |
| Ser Val Leu Leu Pro Thr Tyr Asn Glu Arg Glu Asn Leu Pro Leu Ile |     |
| -25 -20 -15                                                     |     |
| GTG TGG CTG CTG GTG AAA AGC TTC TCC GAG AGT GGA ATC AAC TAT GAA | 195 |
| Val Trp Leu Leu Val Lys Ser Phe Ser Glu Ser Gly Ile Asn Tyr Glu |     |
| -10 -5 1 5                                                      |     |
| ATT ATA ATC ATA GAT GAT GGA AGC CCA GAT GGA ACA AGG GAT GTT GCT | 243 |
| Ile Ile Ile Ile Asp Asp Gly Ser Pro Asp Gly Thr Arg Asp Val Ala |     |
| 10 15 20                                                        |     |
| GAA CAG TTG GAG AAG ATC TAT GGG TCA GAC AGA ATT CTT CTA AGA CCA | 291 |
| Glu Gln Leu Glu Lys Ile Tyr Gly Ser Asp Arg Ile Leu Leu Arg Pro |     |
| 25 30 35                                                        |     |

CGA GAG AAA AAG TTG GGA CTA GGA ACT GCA TAT ATT CDY SRA ATG AAA 339  
Arg Glu Lys Lys Leu Gly Leu Gly Thr Ala Tyr Ile Xaa Xaa Met Lys  
40 45 50

CAT GCA CAG GAA ACT ACA TCA TTA TTA TGG ATS CTG ATC TCT CAC 384  
His Ala Gln Glu Thr Thr Ser Leu Leu Trp Xaa Leu Ile Ser His  
55 60 65

(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 36..268
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 13..245  
id AA134651  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 266..303
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 244..281  
id AA134651  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..272
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 95..353  
id W26888  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..262
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 7..208  
id T66207  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 263..325.  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
                           region 208..270  
                           id T66207  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 39..267  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 1..229  
                           id W00383  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 35..304  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 13..282  
                           id HSC36A071  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 207..266  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.3  
                           seq LLDSSLMASGTAS/RS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

```

AAACCGGGKG TAGACGTACC TCACGGAAGC CGGCTTTGGC CCTGCGGCTK YTACCGTCGC 60
CGCGGAGAAA TTGTTGGATC TGGCAGTCTA GGAATGAATC TCCTCTCAGC CTTTAAGCTC 120
ACCTGGTCAG AATCCTTGGA TGAGCCTGTG GGACCGTTCC TCCTAGCCCG GTGGTTTGGA 180
ACCA GTGGCT TTGGGACTGT AAGAGG ATG GAC AAA GAT TCT CAG GGG CTG CTA 233
 Met Asp Lys Asp Ser Gln Gly Leu Leu
 -20 -15

GAT TCA TCC CTG ATG GCA TCA GGC ACT GCC AGC CGC TCA GAG GAT GAG 281
Asp Ser Ser Leu Met Ala Ser Gly Thr Ala Ser Arg Ser Glu Asp Glu
-10 -5 1 5

GAG TCA CTG GCA GGG CAG AAG CGA GCC TCC TCC CAG GCC CTG GGC ACC 329
Glu Ser Leu Ala Gly Gln Lys Arg Ala Ser Ser Gln Ala Leu Gly Thr
 10 15 20

GGG 332
Gly

```

## (2) INFORMATION FOR SEQ ID NO: 289:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 126..226
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 38..138  
id AA009514  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 252..343
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 161..252  
id AA009514  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..131
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 15..44  
id AA009514  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 100..207
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq CLAVSWEAAGCHG/AG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

AAAGGAATAC TGACAGATAA GGCCGGAAAC AAAACTGATG GCTTGAAAAA CATTTTTATG 60

GAATGTATTT ACTATCATTT TGTTTTACTA TAGAGGTAG ATG GGA CTC TTA ACT 114  
Met Gly Leu Leu Thr  
-35

TTT GGG TAC ATT GAA AMC AKG CKG AAA ACT GAA CAC AAT CCT GAT CAT 162  
Phe Gly Tyr Ile Glu Xaa Xaa Xaa Lys Thr Glu His Asn Pro Asp His  
-30 -25 -20

(A) NAME/KEY: sig peptide



(B) LOCATION: 12..59  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: - score 4.1  
                               seq YAAVAGVLAGVES/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

```

AGCGCGGGAA C ATG GGG CTG TAC GCT GCG GTG GCA GGC GTG CTG GCC GGC 50
 Met Gly Leu Tyr Ala Ala Val Ala Gly Val Leu Ala Gly
 -15 -10 -5

GTG GAG AGC CGC CAG GGC TCT AAT CAA GGG GCT GGT GTA CTC CAG CAA 98
Val Glu Ser Arg Gln Gly Ser Asn Gln Gly Ala Gly Val Leu Gln Gln
 1 5 10

CTT CCA GAA CGT GAA RCA GCT GTA CGC GCT GGT GTG CGA AAS GCA GCG 146
Leu Pro Glu Arg Glu Xaa Ala Val Arg Ala Gly Val Arg Xaa Ala Ala
 15 20 25

CTA CTC CGC CGT GCT GGA TRC CGT GAT CTC CAR CGC CGG CCT CCT CAG 194
Leu Leu Arg Arg Ala Gly Xaa Arg Asp Leu Gln Arg Arg Pro Pro Gln
 30 35 40 45

TGC GAA GAA GCT
Cys Glu Glu Ala
 206

```

(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 299 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Heart

(ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 26..219  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 91  
                               region 1..194  
                               id T06781  
                               est

(ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 204..234  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
                               region 176..206  
                               id T06781  
                               est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 22..74  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 90  
                           region 1..53  
                           id AA101354  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 71..110  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 51..90  
                           id AA101354  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 18..203  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.1  
                           seq LDAVIASAGLLRA/EK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AAAAGGCGCG CGGGAAC ATG GGG CTG TAT GCT GCA GCT GCA GGC GTG TTG  | 50  |
| Met Gly Leu Tyr Ala Ala Ala Ala Gly Val Leu                     |     |
| -60 -55                                                         |     |
| GCC GGC GTG GAG AGC CGC CAG GGC TCT ATC AAG GGG TTG GTG TAC TCC | 98  |
| Ala Gly Val Glu Ser Arg Gln Gly Ser Ile Lys Gly Leu Val Tyr Ser |     |
| -50 -45 -40                                                     |     |
| AGC AAC TTC CAG AAC GTG AAG CAG CTG TAC GCG CTG GTG TGC GAA ACG | 146 |
| Ser Asn Phe Gln Asn Val Lys Gln Leu Tyr Ala Leu Val Cys Glu Thr |     |
| -35 -30 -25 -20                                                 |     |
| CAG CGC TAC TCC GCC GTG CTG GAT GCT GTG ATC GCC AGC GCC GGC CTC | 194 |
| Gln Arg Tyr Ser Ala Val Leu Asp Ala Val Ile Ala Ser Ala Gly Leu |     |
| -15 -10 -5                                                      |     |
| CTC CGT GCG GAG AAG AAG CTG CGG CCG CAC CTG GCC AAG GTG CTA GTG | 242 |
| Leu Arg Ala Glu Lys Lys Leu Arg Pro His Leu Ala Lys Val Leu Val |     |
| 1 5 10                                                          |     |
| TAT GAG TTG TTG TTG GGA AAG GGC TTT CGA GGG GGT GGG GGC CGA TGG | 290 |
| Tyr Glu Leu Leu Leu Gly Lys Gly Phe Arg Gly Gly Gly Gly Arg Trp |     |
| 15 20 25                                                        |     |
| ARG GCC CGG                                                     | 299 |
| Lys Ala Arg                                                     |     |
| 30                                                              |     |

## (2) INFORMATION FOR SEQ ID NO: 292:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 296..458
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..163  
id R50658  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(413..458)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 442..487  
id AA016001  
est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 5..196
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq WLLRLAYLADIFT/KL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| AGAA ATG GGT GCT CAG CAC ACA GCA CTT CTT CTA AAT ACA GAG GTG AGG | 49  |
| Met Gly Ala Gln His Thr Ala Leu Leu Leu Asn Thr Glu Val Arg      |     |
| -60 -55 -50                                                      |     |
| TGG CTT TCT CGA GGT AAA GTT CTT GTA AGA CTT TTT GAA CTT CGT CGT  | 97  |
| Trp Leu Ser Arg Gly Lys Val Leu Val Arg Leu Phe Glu Leu Arg Arg  |     |
| -45 -40 -35                                                      |     |
| GAA CTT TTG GTT TTC ATG GAT TCT GCT TTT CGA CTA TCT GAT TGT TTA  | 145 |
| Glu Leu Leu Val Phe Met Asp Ser Ala Phe Arg Leu Ser Asp Cys Leu  |     |
| -30 -25 -20                                                      |     |
| ACA AAT TCA TCT TGG CTG CTA AGA CTT GCA TAT CTT GCA GAT ATT TTT  | 193 |
| Thr Asn Ser Ser Trp Leu Leu Arg Leu Ala Tyr Leu Ala Asp Ile Phe  |     |
| -15 -10 -5                                                       |     |
| ACT AAA TTA AAT GAA GTT AAT TTG TCA ATG CAA GGA AAA AAT GTG ACC  | 241 |
| Thr Lys Leu Asn Glu Val Asn Leu Ser Met Gln Gly Lys Asn Val Thr  |     |
| 1 5 10 15                                                        |     |
| GTT TTT ACA GTA TTT GAT AAA ATG TCG TCA TTG TTA AGA AAA TTG GAA  | 239 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Phe | Thr | Val | Phe | Asp | Lys | Met | Ser | Ser | Leu | Leu | Arg | Lys | Leu | Glu |     |  |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| TTT | TGG | GCC | TCA | TCT | GTA | GAA | GAA | GAA | AAC | TTT | GAT | TGT | TTT | CCT | ACA | 337 |  |
| Phe | Trp | Ala | Ser | Ser | Val | Glu | Glu | Glu | Asn | Phe | Asp | Cys | Phe | Pro | Thr |     |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| CTC | AGT | GAT | TTT | TTG | ACT | GAA | ATT | AAT | TCT | ACA | GTT | GAT | AAA | GAT | ATT | 385 |  |
| Leu | Ser | Asp | Phe | Leu | Thr | Glu | Ile | Asn | Ser | Thr | Val | Asp | Lys | Asp | Ile |     |  |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| TGC | AGT | GCC | ATT | GTG | CAG | CAC | CTA | AGG | GGT | TTG | CGC | GCT | ACT | CTG | TTA | 433 |  |
| Cys | Ser | Ala | Ile | Val | Gln | His | Leu | Arg | Gly | Leu | Arg | Ala | Thr | Leu | Leu |     |  |
|     |     |     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |  |
| AAA | TAC | TTT | CCT | GTA | ACA | AAT | GAC |     |     |     |     |     |     |     |     | 457 |  |
| Lys | Tyr | Phe | Pro | Val | Thr | Asn | Asp |     |     |     |     |     |     |     |     |     |  |
|     |     |     | 80  |     |     | 85  |     |     |     |     |     |     |     |     |     |     |  |

## (2) INFORMATION FOR SEQ ID NO: 293:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..247
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 19..206  
id AA044042  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 70..247
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 6..183  
id AA127902  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 88..247
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..160  
id AA056679  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(99..247)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 302..450  
id W93399  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 90..237
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 11..158  
id R29154  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 117..191
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq LVVMVPLVGLIHL/GW

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

```

AATCCGCGGC AGAGCGGCTG CTTGAGATCT GTTCTGGGG CCTCTGGCGG TGGCGGCCTG 60
TGGCGGCCTG GGGCGGCGCG ACGGCTGGTG CGCAGGTACA CTGATGCTGA AGTACT ATG 119
 Met
 -25

AGC CTT CGG AAC TTG TGG AGA GAC TAC AAA GTT TTG GTT GTT ATG GTC 167
Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu Val Val Met Val
 -20 -15 -10

CCT TTA GTT GGG CTC ATA CAT TTG GGG TGG TAC AGA ATC AAA AGC AGC 215
Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg Ile Lys Ser Ser
 -5 1 5

CCT GTT TTC CAA ATA CCT AAA AAC GAC AAC ATG 248
Pro Val Phe Gln Ile Pro Lys Asn Asp Asn Met
 10 15

```

## (2) INFORMATION FOR SEQ ID NO: 294:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Heart

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 245..374  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 20..149  
                           id T41381  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 75..227  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.9  
                           seq GKLLQLVLGCAIS/CE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

```

AAAAATAAAA TGTAGGCAGC AAAAGTGGAA GAGGAGAGGC AGCTGGTGCA CTAATCCAGG 60
TCAGCAATCT GAAG ATG GTC TTA CGG AGC CTA GTA GAG TAC TCC CAG GAT 110
 Met Val Leu Arg Ser Leu Val Glu Tyr Ser Gln Asp
 -50 -45 -40

GTC CTG GCG CAT CCT GTG TCA GAA GAG CAT CTC CCA GAT GTG AGC CTC 158
Val Leu Ala His Pro Val Ser Glu Glu His Leu Pro Asp Val Ser Leu
 -35 -30 -25

ATT GGA GAG TTC TCA GAC CCG GCA GAG CTC GGC AAG CTG CTT CAG CTG 206
Ile Gly Glu Phe Ser Asp Pro Ala Glu Leu Gly Lys Leu Leu Gln Leu
 -20 -15 -10

GTG CTG GGC TGT GCC ATC AGT TGC GAG AAA AAG CAG GAC CAC ATC CAG 254
Val Leu Gly Cys Ala Ile Ser Cys Glu Lys Lys Gln Asp His Ile Gln
 -5 1 5

AGA ATC ATG ACG CTG GAA GAA TCG GTT CAG CAT GTG GTG ATG GAA GCC 302
Arg Ile Met Thr Leu Glu Glu Ser Val Gln His Val Val Met Glu Ala
 10 15 20 25

ATC CAA GAG CTC ATG ACC AAA GAC ACT CCT GAC TCC CTG TCA CCA GAG 350
Ile Gln Glu Leu Met Thr Lys Asp Thr Pro Asp Ser Leu Ser Pro Glu
 30 35 40

ACG TAT GGC AAC TTT GAC AGC CAG TCC CGC AGT ACT GGG 389
Thr Tyr Gly Asn Phe Asp Ser Gln Ser Arg Ser Thr Gly
 45 50

```

## (2) INFORMATION FOR SEQ ID NO: 295:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 241..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 105..270  
id AA084830  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 200..229
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 64..93  
id AA084830  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 241..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 66..231  
id W01570  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 200..229
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 26..55  
id W01570  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 296..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..111  
id H82170  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 298..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 7..115  
id N71014  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(147..201)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 238..292  
id N35296  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 358..396
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq MIHGFCLAPTTSA/KN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

```
ATGGGGGCGG ASTAGCCGGA GCCGCGAGTC CATTTTGGGG CTGTGCTTGG CGCGTACCGT 60
GCGGTCCCTG TAGTTGGAGG ACGGGCGGTC GCGCSGGCCT TTCCCACTAG CCGGAGGTCG 120
GAGATAAGTA CCCGCCGCCC GGCTTCTCTC GGGAAAGCGG GGTGGTCCTC GAACCTTCAG 180
CGAGGGTGGG GAGTTGCCCA GTAGCCTCTA GTTCGTTAGT CAAAACGTGA AAAAAAAGA 240
CCTGCTTTGC CVTGGGAAAT AGTAACCCTG CCAAATACAT CAGCTTGTAG GAGACAGAGG 300
ATGTGATGGA GCTGCTTGAA GAAGATCTCA CATGCCCTAT TTGTTGTAGT CTGTTTG 357
ATG ATC CAC GGG TTT TGC CTT GCT CCC ACA ACT TCT GCA AAA AAT GCT 405
Met Ile His Gly Phe Cys Leu Ala Pro Thr Thr Ser Ala Lys Asn Ala
 -10 -5 1
```

## (2) INFORMATION FOR SEQ ID NO: 296:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..86
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 1..63  
id C16698  
est



## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 25..86  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 9..70  
                           id H48377  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 38..86  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 36..84  
                           id R17245  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 38..86  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 7..55  
                           id H19182  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(19..54)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 91  
                           region 181..216  
                           id T12463  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 90..140  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.7  
                           seq RTWCLACVEASPG/QP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

```

AAGCCTGGGA CACCGCCGGC GGGGAGAGAA GCGGATCCCG TCCGAGCCCC GGCCCCAAGT 60
AACGCCGCCG CCCC GGAGCC GCCGTGAGT ATG CYT TGT CCC AGG ACC TGG TGT 113
 Met Xaa Cys Pro Arg Thr Trp Cys
 -15 -10

CTC GCC TGC GTT GAA GCA TCT CCA GGG CAG CCC TTC CTC CCG CCC CGC 161
Leu Ala Cys Val Glu Ala Ser Pro Gly Gln Pro Phe Leu Pro Pro Arg
 -5 1 5

CCC GGG 167
Pro Gly

```

## (2) INFORMATION FOR SEQ ID NO: 297:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 89..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 93..226  
id W81645  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..90
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 31..95  
id W81645  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 89..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 62..195  
id W06951  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..90
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 7..64  
id W06951  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 45..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 2..179  
id W38711  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide

(B) LOCATION: 24..86  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.7  
 seq ETCALASHSGSSG/SK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

```

GCNGTCGGCT CCGCGGCGCC GCC ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC 53
 Met Ala Asp Val Glu Asp Gly Glu Glu Thr
 -20 -15

TGC GCC CTG GCC TCT CAC TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC 101
Cys Ala Leu Ala Ser His Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly
 -10 -5 1 5

GAC AAG ATG TTC TCC CTC AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC 149
Asp Lys Met Phe Ser Leu Lys Lys Trp Asn Ala Val Ala Met Trp Ser
 10 15 20

TGG GAC GTG GAG TGC GAT ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG 197
Trp Asp Val Glu Cys Asp Thr Cys Ala Ile Cys Arg Val Gln Val Met
 25 30 35

GAT GCC TGT MTT AGA TGT CAA GCG GGG 224
Asp Ala Cys Xaa Arg Cys Gln Ala Gly
 40 45

```

(2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 356 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 122..188  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 198..264  
 id R58050  
 est

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(122..188)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 193..259  
 id H98670

est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(122..188)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 194..260  
                           id N66980  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(122..188)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 198..264  
                           id AA159781  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(122..188)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 161..227  
                           id H45410  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 273..350  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.7  
                           seq IIMFLLIIVCGSP/RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

```

TAGAAGTAGC AGGATCGCCT TAATAATAAT AATAGTTTTG TAGCATGAAG CCTGAGCATT 60
GTCCAAAGTT TGGAAATGTG AACGCTGATA GTCACATCTG TCCATCTTTC CACATTTCTA 120
GGATGCTGAC AGACAGCACC AAGAAGTAAT TGCAATTTAT CGGACACACC TTCTTAGTGC 180
TGCACAGGTA AAGAACTACT TCTCCTTTGG AAAGAATATT GCTTTAGAGA TAATAATTTT 240
TATTTTCAAA TAAATTTATG TGAAAGTAAT TG ATG TTT AAA GTA GCT GCA CCC 293
 Met Phe Lys Val Ala Ala Pro
 -25 -20

CCT ATG CTT ATT TAW KAA ATA ATT ATG TTT CTT TTA ATC ATT GTT TGT 341
Pro Met Leu Ile Xaa Xaa Ile Ile Met Phe Leu Leu Ile Ile Val Cys
 -15 -10 -5

GGA TCT CCC AGG CCG
Gly Ser Pro Arg Pro
1

```

356

## (2) INFORMATION FOR SEQ ID NO: 299:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(87..181)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 228..322  
id N29854  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..46)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 363..408  
id N29854  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(44..93)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 315..364  
id N29854  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(87..181)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 67..161  
id T32629  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..93)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 154..246  
id T32629  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: complement(87..181)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 230..324  
id W61289  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(6..93)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 317..404  
id W61289  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(87..181)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 232..326  
id N53422  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(3..93)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 319..409  
id N53422  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 87..181  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 78..172  
id N50275  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 9..93  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 1..85  
id N50275  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 64..126  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.6  
seq FXMCLWSLRNLFS/RC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

```

AGCTATTTGG ATAGTGTAGC TTTAATGTGC TGCACATGAT ACTGGCAGCC CTAGAGTTCA 60
TAG ATG GAC TTT TGG GAC CCA GCA GTT TTT RAA ATG TGT TTA TGG AGT 108
 Met Asp Phe Trp Asp Pro Ala Val Phe Xaa Met Cys Leu Trp Ser
 -20 -15 -10

TTA AGA AAT TTA TTT TCC AGG TGC AGC CCC TGT CTA ACT GAA ATT TCT 156
Leu Arg Asn Leu Phe Ser Arg Cys Ser Pro Cys Leu Thr Glu Ile Ser
 -5 1 5 10

CTT CAC CTT GTA CAC TTG ACA GCT GAA AAA AAA CAA CAT GGG AGT AAT 204
Leu His Leu Val His Leu Thr Ala Glu Lys Lys Gln His Gly Ser Asn
 15 20 25

AAT GGG TCG GCG 216
Asn Gly Ser Ala
 30

```

## (2) INFORMATION FOR SEQ ID NO: 300:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 9..122
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..114  
id R56502  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 173..269
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 162..258  
id R56502  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 129..172
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 119..162  
id R56502

est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 160..261
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6  
seq SVPLLSLSHSIGI/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

```

AGTGACCAAA TGA CTTAACC ACAGATGGAG TGAAGACAGG GGTA ACTGCT TGGTCTGGTC 60
CCCAGTAGAG CATTGCTCAC TATAAACCAC AAGCTGCTTC TAATTTATTT GAGRTGKTAW 120
TAA YCGTGGG CCTTKATATT CTGGTCTCTC TTGCTGCAA ATG AGT CCG GCA GGC 174
 Met Ser Pro Ala Gly
 -30
AAG CAC AAC TCA GAA AGC AAA TTC ACC TTC TTT GTA GCC CTT GAT GGG 222
Lys His Asn Ser Glu Ser Lys Phe Thr Phe Phe Val Ala Leu Asp Gly
 -25 -20 -15
TCG GTC CCC CTG TTG TCT CTT TCT CAT TCC ATA GGC ATT TCC CCC ACA 270
Ser Val Pro Leu Leu Ser Leu Ser His Ser Ile Gly Ile Ser Pro Thr
 -10 -5 1
AGG
Arg
 273

```

## (2) INFORMATION FOR SEQ ID NO: 301:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(78..160)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 149..231  
id H15081  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..71)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98



region 238..308  
id H15081  
- est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(2..71)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 234..303  
id H16744  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(78..160)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 148..230  
id R61691  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(2..72)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 236..306  
id R61691  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(2..85)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 223..306  
id H17833  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(109..160)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 148..199  
id H17833  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 23..73  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq LVCVGLHTEGPWG/RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

ATGTGGTGBT TGTGTCTTAA CT ATG CAC TGG GCC CTT GTC TGC GTC GGC TTG 52  
Met His Trp Ala Leu Val Cys Val Gly Leu

-15

-10

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CAT | ACA | GAG | GGC | CCC | TGG | GGT | CGG | CCC | TCC | GGC | CTG | GCC | TCA | GCC | AGT | 100 |
| His | Thr | Glu | Gly | Pro | Trp | Gly | Arg | Pro | Ser | Gly | Leu | Ala | Ser | Ala | Ser |     |
|     |     | -5  |     |     |     |     | 1   |     |     |     | 5   |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GGG | ATG | GAC | AGG | GCC | AGG | CAG | GCC | TCT | GAA | CTT | CCA | CCT | CCT | GGG | GCC | 148 |
| Gly | Met | Asp | Arg | Ala | Arg | Gln | Ala | Ser | Glu | Leu | Pro | Pro | Pro | Gly | Ala |     |
| 10  |     |     |     |     | 15  |     |     |     | 20  |     |     |     |     | 25  |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| TCC | CAG | ACC | CCC | CAG |     |     |     |     |     |     |     |     |     |     |     | 163 |
| Ser | Gln | Thr | Pro | Gln |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 30  |     |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 302:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 86..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 155..325  
id H16532  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..62
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..58  
id H16532  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 86..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 170..340  
id H17763  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 8..62

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..55  
id H17763  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 86..165  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 168..247  
id R21494  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 11..62  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..52  
id R21494  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 183..222  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 268..307  
id R21494  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 86..238  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 111..263  
id AA084554  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 86..256  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 136..306  
id R52491  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 20..235  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq WFYIGSSLNGTRG/KR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

```

AGAGCTCGCT GTGGCCCGG ATG TTC GGT GCA GCT GCC AGA TCC GCT GAT CTA 52
 Met Phe Gly Ala Ala Ala Arg Ser Ala Asp Leu
 -70 -65

GTG CTT CTC GAA AAA AAC CTT CAG GCG GCC CAT GGG TAT GCC CAA GAG 100
Val Leu Leu Glu Lys Asn Leu Gln Ala Ala His Gly Tyr Ala Gln Glu
-60 -55 -50

GAC AGA GAA CGA ATG CAC AGA DRT ATT GTC AGC CTT GSA CAG AAT CTC 148
Asp Arg Glu Arg Met His Arg Xaa Ile Val Ser Leu Xaa Gln Asn Leu
-45 -40 -35 -30

CTG AAC TTT ATG ATT GGC TCT ATC TTG GAT TTA TGG CAA TGC TTC CTC 196
Leu Asn Phe Met Ile Gly Ser Ile Leu Asp Leu Trp Gln Cys Phe Leu
 -25 -20 -15

TGG TTT TAC ATT GGT TCT TCA TTG AAT GGT ACT CGG GGA AAA AGA GTT 244
Trp Phe Tyr Ile Gly Ser Ser Leu Asn Gly Thr Arg Gly Lys Arg Val
 -10 -5 1

CCA GCG CAC TTT
Pro Ala His Phe
 5

```

## (2) INFORMATION FOR SEQ ID NO: 303:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 3..116
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..114  
id N87112  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..81  
id AA094982  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..130

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..79  
id T68050  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 47..130  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..84  
id AA157180  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 50..130  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..81  
id AA186993  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 43..123  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq VVALLIVCDVPSA/SA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AGCCGGAGCA AAGTTTCACT TATAGAAGGG AGAGGAGCGA AC ATG GCA GCG CGT  | 54  |
| Met Ala Ala Arg                                                 |     |
| -25                                                             |     |
| TGG CGG TTT TGG TGT GTC TCT GTG ACC ATG GTG GTG GCG CTG CTC ATC | 102 |
| Trp Arg Phe Trp Cys Val Ser Val Thr Met Val Val Ala Leu Leu Ile |     |
| -20 -15 -10                                                     |     |
| GTT TGC GAC GTT CCC TCA GCC TCT GCC CGG                         | 132 |
| Val Cys Asp Val Pro Ser Ala Ser Ala Arg                         |     |
| -5 1                                                            |     |

(2) INFORMATION FOR SEQ ID NO: 304:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 436 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 73..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 16..181  
id W32979  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 316..394
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 260..338  
id W32979  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 251..322
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 194..265  
id W32979  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 251..437
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 107..293  
id AA128556  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 145..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..94  
id AA128556  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 251..381
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 104..234  
id T20234  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 153..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 6..91

id T20234

- est

## (ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 383..437

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 235..289  
id T20234  
est

## (ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 115..238

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 65..188  
id T32594  
est

## (ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 251..318

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95  
region 201..268  
id T32594  
est

## (ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 52..115

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 1..64  
id T32594  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 245..292

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.5  
seq LLLQPSMIQEVWT/XY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

```
ATCAGACGCC AGTATAAGCC TTTGAGTCTC AATAGACTGC AGTATCTTAT TGATTGCGGT 60
CGTGTTGATC CTAGTCAACC TATTGACTTA ACCCAGCTTG TCAATGGGAG AGGTGTGACC 120
ATCCAGCCAC TTAAAAGGGA TTATGGTGTC CAGCTGGTTG AGGAGGGTGC TGACACCTTT 180
ACGGCAAAAAG TTAATATTGA AGTACAGTTG GCTTCAGAAC TAGCTATTGC TGCCATTGAA 240
AAAA ATG GTG GTG TTG TTA CTA CAG CCT TCT ATG ATC CAA GAA GTC TGG 289
Met Val Val Leu Leu Leu Gln Pro Ser Met Ile Gln Glu Val Trp
-15 -10 -5
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ACA | THG | TAT | GCA | AAC | CTG | TTC | CAT | TCT | TTC | TTC | GTG | GAC | AAC | CCA | TTC | 337 |
| Thr | Xaa | Tyr | Ala | Asn | Leu | Phe | His | Ser | Phe | Phe | Val | Asp | Asn | Pro | Phe |     |
| 1   |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| CAA | AAA | GAA | TGC | TTC | CAC | CAG | AAG | AAC | TGG | TAC | CAT | ATT | ACA | CTG | ATG | 385 |
| Gln | Lys | Glu | Cys | Phe | His | Gln | Lys | Asn | Trp | Tyr | His | Ile | Thr | Leu | Met |     |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| CAA | AGA | ACC | GTG | GGT | ACC | TGG | CGG | ATC | CTG | CCA | AAT | TTC | CTG | AAG | CAC | 433 |
| Gln | Arg | Thr | Val | Gly | Thr | Trp | Arg | Ile | Leu | Pro | Asn | Phe | Leu | Lys | His |     |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GAC |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 436 |
| Asp |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 305:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 82..407
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 98.5  
region 1..326  
id HSARSE  
vrt

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 88..171
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..84  
id AA160312  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 149..241
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.5  
seq LAVLLSLAPSASS/DI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:



```

AAAACTCGAA GTTAATCATT CCCAGCTCAA AGCCTTGTC AAGTGCTCTC TGCCTTCACG 60
CTTGCTTCCT TTGGGAGAGA ACCTTCCTCT TCTTGATCGG GGATTCAGGA AGGAGCCCAG 120
GRGCAGAGGA AGTAGAGAGA GAGRCAAC ATG TTA CAT CTG CAC CMT TCT TGT 172
 Met Leu His Leu His Xaa Ser Cys
 -30 -25

TTG TGT TTC AGG AGC TGG CTG CCA GCG ATG CTC GCT GTA CTG CTA AGT 220
Leu Cys Phe Arg Ser Trp Leu Pro Ala Met Leu Ala Val Leu Leu Ser
 -20 -15 -10

TTG GCA CCA TCA GCT TCC AGC GAC ATT TCC GCC TCC CGA CCG AAC ATC 268
Leu Ala Pro Ser Ala Ser Ser Asp Ile Ser Ala Ser Arg Pro Asn Ile
 -5 1 5

CTT CTT CTG ATG GCG GAC GAC CTT GGC ATT GGG GAC ATT GGC TGC TAT 316
Leu Leu Leu Met Ala Asp Asp Leu Gly Ile Gly Asp Ile Gly Cys Tyr
 10 15 20 25

GGC AAC AAC ACC ATG AGG ACT CCG ARN ATT GAC CGC CTT GCA GAG GAC 364
Gly Asn Asn Thr Met Arg Thr Pro Xaa Ile Asp Arg Leu Ala Glu Asp
 30 35 40

GGC GTG AAG CTG ACC CAA CAC ATC TCT GCC GCA TCT TTG TGC 406
Gly Val Lys Leu Thr Gln His Ile Ser Ala Ala Ser Leu Cys
 45 50 55

```

## (2) INFORMATION FOR SEQ ID NO: 306:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 15.8  
seq LLLLLLLRHGAQG/KP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

```

Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His
-20 -15 -10 -5

Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala
 1 5

```

## (2) INFORMATION FOR SEQ ID NO: 307:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 14  
seq LAMLALLSPLSLA/QY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

Met Glu Arg Pro Leu Cys Ser His Leu Cys Ser Cys Leu Ala Met Leu  
-25 -20 -15 -10

Ala Leu Leu Ser Pro Leu Ser Leu Ala Gln Tyr Asp Ser Trp Pro Xaa  
-5 1 5

Xaa Pro Glu Tyr Phe Gln Gln Pro  
10 15

## (2) INFORMATION FOR SEQ ID NO: 308:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 12.3  
seq HILFLLLLPVAAA/QT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

Met Ile His Leu Gly His Ile Leu Phe Leu Leu Leu Leu Pro Val Ala  
-15 -10 -5

Ala Ala Gln Thr Thr Pro Gly Glu Arg Ser Ser Leu Pro Ala Phe Tyr  
1 5 10  
Pro Gly Thr Ser Gly Ser Cys Ser Gly Cys Gly Ser Leu Ser Leu Pro  
15 20 25 30  
Leu Leu Ala Gly Leu Val Ala  
35

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -22..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 12.2  
seq LALALGLAQPASA/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

Met Ala Val Lys Leu Gly Thr Leu Leu Leu Ala Leu Ala Leu Gly Leu  
-20 -15 -10

Ala Gln Pro Ala Ser Ala Arg Arg Lys Leu Leu Val Phe Leu Leu  
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -20..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 11.9

seq LVLEFLLLSPVEA/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

```

Met Glu Thr Leu Gly Ala Leu Leu Val Leu Glu Phe Leu Leu Leu Ser
-20 -15 -10 -5

Pro Val Glu Ala Gln Gln Ala Thr Glu His Arg Leu Lys Pro Trp Leu
 1 5 10

Val Gly Leu Ala Ala Val Val Gly Phe Leu Phe Ile Val Tyr Leu Val
 15 20 25

Leu Leu Ala Asn Arg Leu Trp Cys Ser Lys Ala Arg Ala Glu Asp Glu
 30 35 40

Glu Glu Thr Thr Phe Arg Met Glu Ser Gly
45 50

```

(2) INFORMATION FOR SEQ ID NO: 311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.3  
seq PLLSSLLGGSQA/MD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

```

Met Leu Leu Pro Leu Leu Leu Ser Ser Leu Leu Gly Gly Ser Gln Ala
-15 -10 -5

Met Asp Gly Arg Phe Trp Ile Arg Val Gln Glu Ser Val Met Val Pro
1 5 10 15

Glu Gly Leu Cys Ile Ser Val Xaa Leu Leu Phe Leu Leu Pro Pro Thr
 20 25 30

Arg Leu Asp Arg Val Tyr Pro Ser Arg
 35 40

```

(2) INFORMATION FOR SEQ ID NO: 312:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7  
seq LWLLFFLVTAIHA/EL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

```

Met Leu Trp Leu Leu Phe Phe Leu Val Thr Ala Ile His Ala Glu Leu
 -10 -5 1
Cys Gln Pro Gly Ala Glu Asn Ala Phe Lys Val Arg Leu Ser Ile Arg
 5 10 15
Thr Ala Leu Gly Asp Lys Ala Tyr Ala Trp Asp Thr Asn Glu Glu Tyr
 20 25 30
Leu Phe Lys Ala Met Val Ala Phe Ser Met Arg Lys Val Pro Asn Arg
 35 40 45 50
Glu Ala Thr Glu Ile Ser His Val Leu Leu Cys Asn Val Thr Gln Arg
 55 60 65
Val Ser Phe Trp Phe Val Val Thr Asp Pro Ser Lys Asn His Thr Leu
 70 75 80
Pro Ala Val Glu Val Gln Ser Ala Ile Arg Met Asn Lys Asn Arg Ile
 85 90 95
Asn Asn Ala Phe Phe Leu Asn Asp Gln Thr Leu Glu Phe Leu Lys Ile
 100 105 110
Pro Ser Thr Leu Ala Pro Thr Arg
 115 120

```

## (2) INFORMATION FOR SEQ ID NO: 313:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7  
seq LPLLCLFLQGATA/VL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

Met Ala Gly Ser Pro Ser Arg Ala Ala Gly Arg Arg Leu Gln Leu Pro  
-25 -20 -15

Leu Leu Cys Leu Phe Leu Gln Gly Ala Thr Ala Val Leu Phe Ala Val  
-10 -5 1 5

Phe Val Arg Tyr Asn His Lys Thr Asp Ala Ala Leu Trp Xaa Arg Lys  
10 15 20

Leu Gly

## (2) INFORMATION FOR SEQ ID NO: 314:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.6  
seq ALALLLVLP LLWP/CS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

Met Lys Trp Pro Trp Thr Cys Leu Ala Ile Leu Cys Pro Gly Pro Val  
-35 -30 -25

Leu Ser Pro Pro Cys Ser Gly Pro Xaa Leu Ala Leu Ala Leu Leu Leu  
-20 -15 -10

Val Leu Pro Leu Leu Trp Pro Cys Ser Val Phe Gly His Ala Leu Cys  
-5 1 5

Xaa Pro Ser Pro Ala Arg Arg

10

15

## (2) INFORMATION FOR SEQ ID NO: 315:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10  
seq PLLGLLLSLPAGA/DV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

```

Met Pro Ser Trp Ile Gly Ala Val Ile Leu Pro Leu Leu Gly Leu Leu
 -20 -15 -10

Leu Ser Leu Pro Ala Gly Ala Asp Val Lys Ala Arg Ser Cys Gly Glu
 -5 1 5

Val Arg Gln Ala Tyr Gly Ala Lys Gly Phe Ser Leu Ala Asp Ile Pro
 10 15 20 25

Tyr Gln Glu Ile Ala Xaa Glu His Leu Arg Ile Cys Pro Gln Glu Tyr
 30 35 40

Thr Cys Cys Thr Thr Glu Met Glu Asp Lys Leu Ser Gln Gln Ser Lys
 45 50 55

Leu Glu Phe Glu Asn Leu Val Glu Glu Thr Ser His Phe Val Arg Thr
 60 65 70

Thr Phe Val Ser Arg His Lys Lys Phe Asp Gly Arg
 75 80 85

```

## (2) INFORMATION FOR SEQ ID NO: 316:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -28..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 10  
seq LWLSLLVPSCCLCA/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

Met Leu Leu His Trp Val Arg Ser Gln Xaa Xaa Ser Asp Xaa Lys Leu  
-25 -20 -15  
Trp Leu Ser Leu Leu Val Pro Ser Cys Leu Cys Ala Ser Pro Trp Pro  
-10 -5 1  
Leu Pro Ser Leu Pro Leu Leu Leu Pro Pro Ser Leu Leu Ser Leu Leu  
5 10 15 20

(2) INFORMATION FOR SEQ ID NO: 317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -34..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 9.6  
seq LLLFSLLVSPPTC/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

Met Lys Tyr Leu Arg His Arg Arg Pro Asn Ala Thr Leu Ile Leu Ala  
-30 -25 -20  
Ile Gly Ala Phe Thr Leu Leu Leu Phe Ser Leu Leu Val Ser Pro Pro  
-15 -10 -5  
Thr Cys Lys Val Gln Glu Gln Pro Pro Ala Ile Pro Glu Ala Leu Ala  
1 5 10  
Trp Xaa Thr Pro Pro Thr Arg Trp  
15 20



## (2) INFORMATION FOR SEQ ID NO: 318:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.5  
seq AMWWLLLWGVLQA/WP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

```

Met Pro Gly Pro Arg Val Trp Gly Lys Tyr Leu Trp Arg Ser Pro His
-35 -30 -25 -20

Ser Lys Gly Cys Pro Gly Ala Met Trp Trp Leu Leu Leu Trp Gly Val
 -15 -10 -5

Leu Gln Ala Trp Pro Xaa Pro Gly Leu Arg Pro Leu Gly Pro Arg Ala
 1 5 10

Thr Pro Ala Ala Asp Ile Pro Arg Val Pro Arg Ala Val Trp Gln Arg
 15 20 25

Pro Arg Glu Gln His Gly His Gln Gly Ser Arg Gly Leu Cys Cys Glu
 30 35 40 45

Ala Arg Leu Pro Gly Leu Arg Pro Gly Ala Val Pro Gly Leu Cys Arg
 50 55 60

Gly Leu Xaa Xaa Asn Leu Ile Arg Arg Phe Gly Ser Lys Pro Val Leu
 65 70 75

Trp Ser Ala Arg Leu Pro Ser Gly Gln Ala Pro Trp Ser Glu Gly
 80 85 90

```

## (2) INFORMATION FOR SEQ ID NO: 319:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.2  
seq LLAVLLASWRLWA/IK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

```

Met Cys Gly Pro Ala Met Phe Pro Ala Gly Pro Pro Trp Pro Arg Val
 -35 -30 -25

Arg Val Val Gln Val Leu Trp Ala Leu Leu Ala Val Leu Leu Ala Ser
 -20 -15 -10

Trp Arg Leu Trp Ala Ile Lys Asp Phe Gln Glu Cys Thr Trp Gln Val
 -5 1 5 10

Val Leu Asn Glu Phe Lys Arg Val Gly Glu Ser Gly Val Ser Asp Xaa
 15 20 25

Ser Leu Ser Lys Ser Pro Gly
 30

```

## (2) INFORMATION FOR SEQ ID NO: 320:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -55..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.2  
seq SLLLLSTALNILA/CQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

```

Met His Arg Arg Lys Leu Pro Leu Thr Asn Lys Arg Gln Leu Gln Lys
-55 -50 -45 -40

Xaa Leu Ser Lys Phe Ile Phe Ser Asp Glu Leu Phe Arg Asn Ile Leu
 -35 -30 -25

Phe Ser Leu Arg Thr Leu Arg Met Ile Leu Ser Leu Leu Leu Ser

```

-20

-15

-10

Thr Ala Leu Asn Ile Leu Ala Cys Gln Ile Asn Glu Glu Leu Gly  
-5 1 5

## (2) INFORMATION FOR SEQ ID NO: 321:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3  
seq VSALLMAWFGVLS/CV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

Met Lys Leu Trp Val Ser Ala Leu Leu Met Ala Trp Phe Gly Val Leu  
-15 -10 -5

Ser Cys Val Gln Ala Xaa Xaa  
1 5

## (2) INFORMATION FOR SEQ ID NO: 322:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.1  
seq LCLVCLLVHTAFR/VV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

Met Gln Leu Pro Leu Ala Leu Cys Leu Val Cys Leu Leu Val His Thr  
                               -15                              -10                              -5

Ala Phe Arg Val Val Glu Gly Gln Gly Trp Gln Ala Phe Lys Asn Asp  
                               1                                              5                                              10

Ala Thr Glu Ile Ile Pro Glu Leu Gly Glu Tyr Pro Glu Pro Pro Pro  
           15                                              20                                              25

Glu Arg  
   30

## (2) INFORMATION FOR SEQ ID NO: 323:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8  
seq ILLCSVAVXLSPS/EP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

Met Leu Cys Ile His Xaa Xaa Arg Ile Ile Gln Asp Ser Phe Ile Ala  
       -30                              -25                              -20

Leu Lys Ile Leu Leu Cys Ser Val Ala Val Xaa Leu Ser Pro Ser Glu  
       -15                              -10                              -5                              1

Pro Leu Ala Pro  
                               5

## (2) INFORMATION FOR SEQ ID NO: 324:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -38..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.9  
seq LPFLSLFWPWAPG/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

|     |           |            |            |           |     |          |            |            |           |          |     |            |            |           |           |
|-----|-----------|------------|------------|-----------|-----|----------|------------|------------|-----------|----------|-----|------------|------------|-----------|-----------|
| Met | Gly       | Gly        | Phe<br>-35 | Phe       | Pro | Pro      | Thr        | Glu<br>-30 | Val       | Arg      | Glu | Val        | Cys<br>-25 | Ala       | Asn       |
| Gln | Gly       | Ala<br>-20 | Ala        | His       | Asn | Arg      | Asp<br>-15 | Arg        | Leu       | Pro      | Phe | Leu<br>-10 | Ser        | Leu       | Phe       |
| Trp | Pro<br>-5 | Trp        | Ala        | Pro       | Gly | Ala<br>1 | Val        | Ser        | Val       | Gly<br>5 | Gln | Ala        | Arg        | Tyr       | Arg<br>10 |
| Thr | Pro       | Thr        | Thr        | Xaa<br>15 | Ala | Pro      | Ser        | Ala        | Ser<br>20 | Val      | Pro | Trp        | Pro        | Arg<br>25 | Ala       |
| Gly | Thr       | Cys        | Arg<br>30  | Thr       | Pro | Thr      |            |            |           |          |     |            |            |           |           |

(2) INFORMATION FOR SEQ ID NO: 325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -30..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.9  
seq HLWILLLFSEFCWM/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

Met Lys Leu Phe Tyr Asn Gln Leu Val Ser Glu Thr Lys His Asp Phe  
-30 -25 -20 -15  
Ala His Leu Trp Ile Leu Leu Leu Phe Ser Phe Cys Trp Met Ser Arg  
-10 -5 1  
Ser Phe Phe Phe Phe  
5

## (2) INFORMATION FOR SEQ ID NO: 326:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9  
seq LLFFHILFHSCFS/HL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

Met Pro Ser Glu Ser Pro Pro Leu Leu Phe Phe His Ile Leu Phe His  
-20 -15 -10 -5

Ser Cys Phe Ser His Leu Leu  
1

## (2) INFORMATION FOR SEQ ID NO: 327:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -68..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9  
seq LLCSALAWQQSLS/GK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

Met Ser Ser Met Trp Ser Glu Tyr Thr Ile Gly Gly Val Lys Ile Tyr  
-65 -60 -55

Phe Pro Tyr Lys Ala Tyr Pro Ser Gln Leu Ala Met Met Asn Ser Ile

-50

-45

-40

Leu Arg Gly Leu Asn Ser Lys Gln His Cys Leu Leu Glu Ser Pro Thr  
 -35 -30 -25

Gly Ser Gly Lys Ser Leu Ala Leu Leu Cys Ser Ala Leu Ala Trp Gln  
 -20 -15 -10 -5

Gln Ser Leu Ser Gly Lys Pro Ala Asp Glu Gly Val Ser Glu Lys Ala  
 1 5 10

Glu Val Gln Leu Ser Cys Cys Cys Ala Cys His Ser Lys Asp Phe Thr  
 15 20 25

Asn Asn Asp Met Asn Gln Gly Thr Ser Arg His Phe Asn Tyr Pro Ser  
 30 35 40

Thr Pro Arg  
 45

(2) INFORMATION FOR SEQ ID NO: 328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8  
seq FVRFGLGFVSCLQS/DP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

Met Ala Leu Phe Leu Glu Leu Phe Leu Asn Ser Tyr Ser Leu Leu Phe  
 -25 -20 -15

Val Arg Phe Leu Gly Phe Val Ser Cys Leu Gln Ser Asp Pro Ile Cys  
 -10 -5 1

Ser Phe Phe Phe Phe  
 5

(2) INFORMATION FOR SEQ ID NO: 329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids

(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -24..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.8  
seq LMAGSSLSAGVSG/ED

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

Met Asn Glu Asp Glu Lys Glu Met Lys Glu Ile Leu Met Ala Gly Ser  
                  -20                  -15                  -10  
Ser Leu Ser Ala Gly Val Ser Gly Glu Asp Lys Thr Glu Ile Leu Asn  
                  -5                          1                          5  
Pro Thr Pro Xaa Met Ala Lys Ser Leu Thr Ile Asp Cys Leu Glu Leu  
          10                          15                          20  
Ala Leu Pro Pro Glu Leu Ala Phe Gln Leu Asn Glu Leu Phe Gly Pro  
  25                          30                          35                          40  
Val Gly Ile Asp Ser Gly Ser Leu  
                          45

(2) INFORMATION FOR SEQ ID NO: 330:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -21..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.8  
seq IIPLIXXLSLCLC/LW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

Met Gly Ser Phe Leu Leu Gly Gly Ile Ile Pro Leu Ile Xaa Xaa Leu



-20

-15

-10

Ser Leu Cys Leu Cys Leu Trp Trp Arg Ile Ile  
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 331:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig peptide

(B) LOCATION: -31..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7.8

seq VCLLCSGCSCAWS/VG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

Met Leu Gln Val Ala Thr Thr Asn Tyr Leu Glu Leu Ala Arg Glu Val  
-30 -25 -20

Lys Pro Val Cys Leu Leu Cys Ser Gly Cys Ser Cys Ala Trp Ser Val  
-15 -10 -5

Gly Cys Val Xaa Glu Ser Glu Ser Glu  
5 10

(2) INFORMATION FOR SEQ ID NO: 332:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig peptide

(B) LOCATION: -18..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7.7

seq PFFLALCFPKSTS/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

Met Phe Cys Leu Ala Pro Phe Phe Leu Ala Leu Cys Phe Pro Lys Ser  
           -15                                  -10                                  -5

Thr Ser Gln Pro Gln Arg  
           1

(2) INFORMATION FOR SEQ ID NO: 333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.5  
seq QCLCCISPPVFC/EG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

Met Ser Glu Ser Arg Phe Gln Pro Gln Asn Gln Gly Gly Ser Leu Gln  
           -30                                  -25                                  -20

Leu Pro Leu Gln Cys Leu Leu Cys Cys Ile Ser Pro Pro Val Phe Cys  
           -15                                  -10                                  -5

Glu Gly Asn Trp Leu Ser Tyr Phe Tyr Val Leu Pro Gly Phe Val Cys  
       1                                  5                                  10                                  15

Glu Leu His Lys Leu Gly Ile Ser Cys Leu Ile Pro Leu Phe Ser Val  
           20                                  25                                  30

Ser Pro Leu Ala Ala Trp Met Val  
           35                                  40

(2) INFORMATION FOR SEQ ID NO: 334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -23..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.3  
seq SSCLLGLLHLSSQ/FS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

Met Pro Lys His Cys His Ser Phe Ile Thr Ser Ser Cys Leu Leu Gly  
-20 -15 -10  
Leu Leu His Leu Ser Ser Gln Phe Ser Cys Pro Gly Arg Lys Leu His  
-5 1 5  
Pro Ala Gln Arg His Thr Glu Ala Glu Thr Gln Gly Arg Pro Leu Ser  
10 15 20 25  
Asp Arg

(2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -19..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.2  
seq FIXFPFLFPFSFS/QT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

Met Cys Leu Leu Phe Xaa Phe Ile Xaa Phe Pro Phe Leu Phe Pro Phe  
-15 -10 -5  
Ser Phe Ser Gln Thr Phe Ser Phe Ser Gln His Trp Asn Thr Gly Gly  
1 5 10  
Ser His Pro Glu Glu Leu Glu Arg Pro Gly Ala His Pro Arg Leu Lys  
15 20 25

Ala Arg Pro Gln Pro Pro Leu Phe His Pro Phe Ile Ser Ser  
 30 35 40

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1  
seq LLVASGXAEGVSA/QS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

Met Ala Ser Glu Arg Xaa Pro Asn Arg Pro Xaa Cys Leu Leu Val Ala  
 -25 -20 -15 -10

Ser Gly Xaa Ala Glu Gly Val Ser Ala Gln Ser Phe Leu Xaa Cys Phe  
 -5 1 5

Thr Met Ala Ser Thr Xaa Phe Asn Leu Gln Val Ala Xaa Pro Gly Gly  
 10 15 20

Lys Ala Met Glu Phe Val Asp Val Thr Xaa Ser Asn Ala Arg Trp Val  
 25 30 35

Gln Asp  
 40

(2) INFORMATION FOR SEQ ID NO: 337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -25..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.1  
 seq LAFQLVFLRATSG/SC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

Met Phe Pro Asp Tyr Lys Leu Gly Gly Ser Tyr Leu Leu Ala Phe Gln  
 -25 -20 -15 -10  
 Leu Val Phe Leu Arg Ala Thr Ser Gly Ser Cys Ser Lys Tyr Arg Arg  
 -5 1 5  
 His Leu His Asn Ile Asn Val Arg Pro Gly Leu Val Arg Leu Leu Gly  
 10 15 20  
 Ser Cys Ile Gln Lys Gln Pro Gly  
 25 30

(2) INFORMATION FOR SEQ ID NO: 338:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -25..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.1  
 seq LLLXLXLLLLIALE/IM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

Met Arg Arg Ile Ser Leu Thr Ser Ser Pro Val Arg Leu Leu Leu Xaa  
 -25 -20 -15 -10  
 Leu Xaa Leu Leu Leu Ile Ala Leu Glu Ile Met Val Gly Gly His Ser  
 -5 1 5  
 Leu Cys Phe Asn Phe Thr Ile Lys Ser Leu Ser Arg Pro Gly Gln Pro  
 10 15 20  
 Trp Cys Glu Ala His Val Phe Leu Asn Lys Asn Leu Phe Leu Gln Tyr  
 25 30 35  
 Asn Ser Asp Asn Asn Met Val Lys Pro Leu Gly Leu Leu Gly Lys Lys  
 40 45 50 55

Val Tyr Ala Thr Ser Thr Trp Gly Glu Leu Thr Gln Thr Leu Gly Glu  
60 65 70

Val Gly Arg Asp Leu Arg Met Leu Leu Cys Asp Ile Lys  
75 80

(2) INFORMATION FOR SEQ ID NO: 339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq TFLLLLFNXNAGRS/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

Met Thr Phe Leu Leu Leu Phe Xaa Asn Ala Gly Arg Ser Leu Arg  
-10 -5 1

Met Cys

(2) INFORMATION FOR SEQ ID NO: 340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq EMFLVLLVTGVHS/NK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

Met Arg Thr Val Val Leu Thr Met Lys Ala Ser Val Ile Glu Met Phe  
 -25 -20 -15

Leu Val Leu Leu Val Thr Gly Val His Ser Asn Lys Glu Thr Ala Lys  
 -10 -5 1 5

Lys Ile Lys Arg Pro Gly  
 10

(2) INFORMATION FOR SEQ ID NO: 341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9  
seq ISLLFIFFSIANS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

Met Ser Ser Pro Leu Leu Val Glu Gln Ser Ser Thr Lys Ser Pro Lys  
 -40 -35 -30 -25

Ser Trp Ser Trp Ser Phe Leu Ala Phe Ser Cys Ile Ser Leu Leu Phe  
 -20 -15 -10

Ile Phe Phe Ser Ile Ala Asn Ser Ser Pro Cys Gly  
 -5 1

(2) INFORMATION FOR SEQ ID NO: 342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9  
seq IPLLLLFFHLSFL/NS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

```

Met Tyr Leu Phe Cys Leu Phe Ser Val Ser Lys Thr Ile Pro Leu Leu
-25 -20 -15 -10

Leu Leu Phe Phe His Leu Ser Phe Leu Asn Ser Leu
 -5 1

```

## (2) INFORMATION FOR SEQ ID NO: 343:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9  
seq CLLILKFLSPAET/SI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

```

Met Ile Val Cys Leu Leu Ile Leu Lys Phe Leu Ser Pro Ala Glu Thr
-15 -10 -5

Ser Ile Leu Ser Ser Ile Ala Thr Tyr Gly Ala Phe Tyr Phe Ile Val
 1 5 10 15

Pro Leu Glu Val Ser Gln Ile Leu Gln Thr Gln
 20 25

```

## (2) INFORMATION FOR SEQ ID NO: 344:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR



(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7  
seq LILCFLFILHTHT/HT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

Met Asp Lys Ser Ile Lys Ser Ser Ile Ile Trp Ser Leu Ile Leu Cys  
-25 -20 -15 -10

Phe Leu Phe Ile Leu His Thr His Thr His Thr His Thr His  
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7  
seq IFDLLLLLXXSNQ/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

Met Phe Phe Ile Phe Ile Asn Gly Phe Thr Leu Leu Leu Met Thr Leu  
-35 -30 -25

Ala Met Lys Pro Arg His Pro Ile Phe Asp Leu Leu Leu Leu Xaa  
-20 -15 -10 -5

Xaa Ser Asn Gln Leu Pro Val Thr Gly  
1 5

(2) INFORMATION FOR SEQ ID NO: 346:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -60..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7  
seq LWPFLTWINPALS/IC

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

Met Cys Pro Ser Leu Glu Glu Ala Pro Ser Val Lys Gly Thr Leu Pro  
-60 -55 -50 -45

Cys Ser Gly Gln Gln Gln Pro Phe Pro Phe Gly Ala Ser Asn Ile Pro  
-40 -35 -30

Leu Leu Leu Gly Arg Ser Arg Lys Val Ala Arg Gly Ala Pro Val Leu  
-25 -20 -15

Trp Pro Phe Leu Thr Trp Ile Asn Pro Ala Leu Ser Ile Cys Asp Pro  
-10 -5 1

Leu Gly Ser Cys Gly Trp Gln  
5 10

## (2) INFORMATION FOR SEQ ID NO: 347:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6  
seq LLSALWFCHPCCL/CC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

```

Met Leu Gln Asp Leu Leu Ser Ala Leu Trp Phe Cys His Pro Cys Cys
 -15 -10 -5

Leu Cys Cys Gly Leu Cys Trp Leu Gly Val Asp Ala Gly Cys Ser Gln
 1 5 10 15

Gly Gly Ser Gly Cys Pro
 20

```

(2) INFORMATION FOR SEQ ID NO: 348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6  
seq LLSLAAYLSGPHQ/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

```

Met Met Asp Leu Arg Pro Leu Leu Ser Leu Ala Ala Tyr Leu Ser Gly
 -15 -10 -5

Pro His Gln Glu Pro Ser Val Pro Thr Arg Asp Gly Asp Val Asn Asn
 1 5 10

Leu Pro Lys Pro Asn Pro Ala Arg Ser Val Lys Gln Gly Gly Ile Trp
 15 20 25

Lys Ala Glu Gln Glu Arg Val Glu Val Glu
 30 35

```

(2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -19..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.6  
seq LLPGLPLVRTSFS/HF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

Met Glu Met Pro Pro Cys Leu Leu Pro Gly Leu Pro Leu Val Arg Thr  
                  -15                  -10                  -5

Ser Phe Ser His Phe Phe Ser Leu Ser Gly Gly Thr Thr Thr Ala Arg  
                  1                  5                  10

Gly

## (2) INFORMATION FOR SEQ ID NO: 350:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -25..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.5  
seq GLAMLVHTRGVXG/SR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

Met Thr Val Glu Leu Trp Leu Arg Leu Arg Gly Lys Gly Leu Ala Met  
-25                  -20                  -15                  -10

Leu His Val Thr Arg Gly Val Xaa Gly Ser Arg Val Arg Val Xaa Xaa  
                  -5                  1                  5

Xaa Leu Pro Ala Leu Leu Gly Xaa Pro Arg Ala Leu Ser Ser Xaa Ala  
                  10                  15                  20

Ala Lys Met Gly Xaa Tyr Arg Xaa Met Trp  
                  25                  30

## (2) INFORMATION FOR SEQ ID NO: 351:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.4  
seq LLILLCSSPPDRV/SY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

Met Ser Ile Glu Asp Phe Val Asn Arg Ser Ile Leu Leu Ile Leu Leu  
                  -20                  -15                  -10

Cys Ser Ser Pro Pro Asp Arg Val Ser Tyr Arg Ala Lys Val Leu His  
                  -5                          1                          5

Ser Leu Leu Gln Leu Pro Ala Gln  
          10                          15

## (2) INFORMATION FOR SEQ ID NO: 352:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.4  
seq FALLFLFLVPVPG/HG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

Met Arg Ile His Tyr Leu Leu Phe Ala Leu Leu Phe Leu Phe Leu Val  
-20                  -15                          -10                          -5

Pro Val Pro Gly His Gly Gly Ile Ile Asn Thr Leu Gln Lys Tyr Xaa

1                                  5                                  10

Leu Gln Ser Gln Arg Arg Pro Val Cys Cys Ala Gln Leu Pro Ser Lys  
15                                  20                                  25

Gly Glu Arg  
30

(2) INFORMATION FOR SEQ ID NO: 353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -13..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.4  
seq MCLLTALVTOVIS/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

```

Met Cys Leu Leu Thr Ala Leu Val Thr Gln Val Ile Ser Leu Arg Lys
 -10 -5 1
Asn Ala Glu Arg Thr Cys Leu Cys Lys Arg Arg Trp Pro Trp Xaa Pro
 5 10 15
Ser Pro Arg Ile Tyr Cys Ser Ser Thr Pro Cys Asp Ser Lys Phe Pro
 20 25 30 35
Thr Val Tyr Ser Ser
 40

```

(2) INFORMATION FOR SEQ ID NO: 354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq GLALVAGTPPSRS/CP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

Met Met Gly Asn Pro Gly Leu Ala Leu Val Ala Gly Thr Pro Pro Ser  
           -15                          -10                          -5

Arg Ser Cys Pro Gln Ala Asn Ser Gln Thr Arg  
           1                              5

## (2) INFORMATION FOR SEQ ID NO: 355:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -38..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq PCVSLLWAPRXFA/SS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

Met Asn His Leu Met Pro Leu Thr Val Leu His Ser Val Leu Glu Met  
           -35                          -30                          -25

Leu Arg Thr Pro Arg Thr Pro Pro Trp Pro Cys Val Ser Leu Leu Trp  
           -20                          -15                          -10

Ala Pro Arg Xaa Phe Ala Ser Ser Cys Ser Gln Ala Phe Thr Thr Leu  
           -5                              1                              5                              10

Xaa Xaa Asn Cys Leu Leu Thr Asn Pro Ser Pro Thr Leu Asp Cys Asp  
                           15                              20                              25

Leu Pro Glu Gly Ser Glu Ile Leu Asn Ser Ser Leu Tyr Pro His Cys  
           30                              35                              40

Leu Leu Ser Ala Trp Asn Thr Arg His Ser Thr  
           45                              50

(2) INFORMATION FOR SEQ ID NO: 356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -24..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.3  
seq SLXLRLASQLSEG/DT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

Met Gly His Val Val Phe Gly Asp Ile Lys Asn Ser Leu Leu Xaa Leu  
-20 -15 -10

Arg Ala Ser Gln Leu Ser Glu Gly Asp Thr Xaa Xaa Xaa Xaa Cys Pro  
-5 1 5

Xaa Met Xaa Arg Gly Lys His Ile Ser Tyr  
10 15

## (2) INFORMATION FOR SEQ ID NO: 357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Heart

(ix) FEATURE:

- ```
{A} NAME/KEY: sig_peptide
{B} LOCATION: -81..-1
{C} IDENTIFICATION METHOD: Von Heijne matrix
{D} OTHER INFORMATION:  score 6.3
                        seq FLSLLXSVSETPG/SL
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

Met Ala Gly Gly Arg Arg Asp Tyr Ser Gln Leu Phe Gly Arg Gly Pro
-30 -75 -70

Gly Arg Leu Ser Arg Ala Arg Ala Ser Val Val Arg Trp Ser Pro Arg
 -65 -60 -55 -50
 Ala Thr Ala Cys Pro Ala Pro Pro Ser Leu Pro Asp Leu Lys Arg Gln
 -45 -40 -35
 Glu Leu Val Ser Arg Ile Glu Cys Gly Cys Arg Gly Pro Val Gly Ala
 -30 -25 -20
 Thr Ala Asp Phe Phe Leu Ser Leu Leu Xaa Ser Val Ser Glu Thr Pro
 -15 -10 -5
 Gly Ser Leu Arg Xaa Asn Asp Leu Phe Phe Val Ser Gln Leu Ile Trp
 1 5 10 15
 Gly Arg

(2) INFORMATION FOR SEQ ID NO: 358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1
seq LWCFHSFISFSL/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

Met Phe Trp Xaa Gly Ser Leu Trp Cys Phe His Ser Phe Ile Ser Phe
 -15 -10 -5
 Ser Leu Ser Ser Ser Arg
 1

(2) INFORMATION FOR SEQ ID NO: 359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6
seq FLLTFFSYSLHA/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

Met Ala Trp Pro Asn Val Phe Gln Xaa Gly Ser Leu Leu Ser Gln Phe
-35 -30 -25

Xaa Xaa His His Val Val Val Phe Leu Leu Thr Phe Phe Ser Tyr Ser
-20 -15 -10 -5

Leu Leu His Ala Ser Arg Lys Thr Phe Xaa Asn Val Lys Val Ser Ile
1 5 10

Ser Glu Gln Trp Thr Pro Ser Ala Phe Asn Thr Ser Val Glu Leu Pro
15 20 25

Val Glu Ile Trp Ser Ser Xaa His Leu Phe Pro Ser Ala Glu
30 35 40

(2) INFORMATION FOR SEQ ID NO: 360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6
seq WILAVGLSLPSSS/XI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

Met Ile Leu Arg Asn Leu Trp Ile Leu Ala Val Gly Leu Ser Leu Pro
-15 -10 -5

Ser Ser Ser Xaa Ile Lys Phe His Phe Ser Leu Tyr Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq LCGLLHLWLKVFS/LK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

Met Leu Thr Val Asn Asp Val Arg Phe Tyr Arg Asn Val Arg Ser Asn
-35 -30 -25 -20

His Phe Pro Phe Val Arg Leu Cys Gly Leu Leu His Leu Trp Leu Lys
 -15 -10 -5

Val Phe Ser Leu Lys Gln Leu Lys Lys
 1 5

(2) INFORMATION FOR SEQ ID NO: 362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq LFLNLCILAXPFS/KQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

```

Met Asn Leu Lys Pro Gly Leu Pro Cys Asn Leu Phe Leu Asn Leu Cys
    -20                      -15                      -10

Ile Leu Ala Xaa Pro Phe Ser Lys Gln Ile Ile Glu Leu Leu Glu Tyr
    -5                      1                      5

Val Ser Tyr His Pro Cys Val Leu Val Tyr Ser Glu Tyr Xaa Asn Ile
    10                      15                      20                      25

Ser Ile Val Tyr Thr Leu
                      30

```

(2) INFORMATION FOR SEQ ID NO: 363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq VVLAWGLLNVSMA/GM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

```

Met Met Gln Gly Glu Ala His Pro Ser Ala Ser Leu Ile Asp Arg Thr
-40                      -35                      -30                      -25

Ile Lys Met Arg Lys Glu Thr Glu Ala Arg Lys Val Val Leu Ala Trp
    -20                      -15                      -10

Gly Leu Leu Asn Val Ser Met Ala Gly Met Ile Tyr Thr Glu Met Thr
    -5                      1                      5

Gly Lys Leu Ile Ser Ser Tyr Tyr Asn Val Thr Tyr Trp Pro Leu Trp
    10                      15                      20

Tyr Xaa Glu Leu Ala Leu Ala Ser Leu Phe Ser Leu Asn Ala Leu Phe
    25                      30                      35                      40

Asp Phe Trp Arg Tyr Phe Lys Tyr Thr Val Ala Pro Thr Ser Leu Val
    45                      50                      55

Val Ser Pro Gly Arg
    60

```

(2) INFORMATION FOR SEQ ID NO: 364:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -19..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.9

seq PXXLLILAHITQS/CP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

Met Met Asn Gln Thr His Pro Xaa Xaa Leu Leu Ile Leu Ala His Ile
-15 -10 -5

Thr Gln Ser Cys Pro Trp Ala His Val Gly Ala Ala Pro Ser Ala Leu
1 5 10

Leu Ile His Arg Trp Glu Leu Arg Gly Cys Ser Tyr Leu Lys Leu Phe
15 20 25

Leu Val Met Val Leu Ile Phe Glu Met Leu
30 35

(2) INFORMATION FOR SEQ ID NO: 365:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig peptide

(B) LOCATION: -20..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.8

seq GLVLLSLAEILF/KI

(X1) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

Met Gly Leu Pro Glu Arg Arg Gly Leu Val Leu Leu Leu Ser Leu Ala
 -20 -15 -10 -5

Glu Ile Leu Phe Lys Ile Met Ile Leu Glu Gly Gly Gly Val Met Asn
 1 5 10

Leu Asn Pro Gly Asn Asn Leu Leu His Gln Pro Pro Ala Trp Thr Asp
 15 20 25

Ser Tyr Ser Thr Cys Asn Val Ser Ser Gly Phe Phe Gly Gly Gln Trp
 30 35 40

His Glu Ile His Pro Gln Tyr Trp Thr Lys Tyr Gln Val Trp Glu Trp
 45 50 55 60

Leu Gln His Leu Leu Asp Thr Asn Gln Leu Asp Ala Asn Cys Ile Pro
 65 70 75

Phe Gln Glu Phe Asp Ile Asn Gly Glu Xaa Arg
 80 85

(2) INFORMATION FOR SEQ ID NO: 366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8
seq LCWALLYNCFSSS/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

Met Trp Gly Leu Glu Glu Asp Arg Ser Tyr Gln Gly Leu Arg Pro Leu
 -25 -20 -15

Cys Trp Ala Leu Leu Tyr Asn Cys Phe Ser Ser Ser Cys Val Pro Val
 -10 -5 1

Ala Leu Val
 5

(2) INFORMATION FOR SEQ ID NO: 367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -85..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq ALLASLGIAFSRS/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

Met Leu Cys Arg Asp Gly Ser Ala Cys Val Pro Arg Ser Arg Arg Leu
-85 -80 -75 -70
Pro Leu Pro Ala Ala Val Arg Ala His Gly Pro Met Ala Asp Xaa Xaa
-65 -60 -55
Asp Ser Ala Arg Gly Cys Val Val Phe Glu Asp Val Phe Val Tyr Phe
-50 -45 -40
Ser Arg Glu Glu Trp Glu Leu Leu Asp Asp Ala Gln Arg Leu Leu Tyr
-35 -30 -25
His Asp Val Met Leu Glu Asn Phe Ala Leu Leu Ala Ser Leu Gly Ile
-20 -15 -10
Ala Phe Ser Arg Ser Arg Ala Val Met Lys Leu
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -56..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.7
seq FLCFLNLTSHLSG/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

```

Met Leu Ile Thr Arg Leu Gln Ser Gly Ile Asp Phe Ala Ile Gln Leu
-55                      -50                      -45

Asp Glu Ser Thr Asp Ile Gly Ser Cys Thr Thr Leu Leu Val Tyr Val
-40                      -35                      -30                      -25

Arg Tyr Ala Trp Gln Asp Asp Phe Leu Glu Asp Phe Leu Cys Phe Leu
                -20                      -15                      -10

Asn Leu Thr Ser His Leu Ser Gly Leu Asp Ile Phe Thr Glu Leu Glu
                -5                      1                      5

Arg Arg Gly
10

```

(2) INFORMATION FOR SEQ ID NO: 369:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -38..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.7
seq LAFLSCLAFLVLD/TQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

```

Met Glu Ser Pro Gln Leu His Cys Ile Leu Asn Ser Asn Ser Val Ala
                -35                      -30                      -25

Cys Ser Phe Ala Val Gly Ala Gly Phe Leu Ala Phe Leu Ser Cys Leu
                -20                      -15                      -10

Ala Phe Leu Val Leu Asp Thr Gln Glu Thr Arg Ile Ala Gly Thr Arg
                -5                      1                      5                      10

Phe Lys Thr Ala Phe Gln Leu Leu Asp Xaa Ile Leu Ala Val Leu Trp
                15                      20                      25

```


(2) INFORMATION FOR SEQ ID NO: 370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq DHLFLLFPRSCSS/LV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

Met Ser Asn Lys Tyr Ile Lys Pro Ser Met Ser Pro Gly Asn Thr Asp
-25 -20 -15
His Leu Phe Leu Leu Phe Pro Arg Ser Cys Ser Ser Leu Val
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq FFFFLFLLPPXPP/TG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

Met Val Glu Leu Lys Gln Leu Gly Pro Arg Ser Phe Phe Phe Phe Leu
-20 -15 -10
Phe Leu Leu Pro Pro Xaa Pro Pro Thr Gly
-5 1

(2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq LILPALFFFPLHC/TF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

Met Pro Tyr Val Thr Ile Pro Tyr Ile Ile Val Tyr Ser Leu Ile Leu
-25 -20 -15

Pro Ala Leu Phe Phe Phe Pro Leu His Cys Thr Phe His Gly Leu Thr
-10 -5 1 5

Tyr Tyr Ile Ser Cys Val Cys Ser Leu Ser Leu Pro Thr
10 15

(2) INFORMATION FOR SEQ ID NO: 373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq LLLCMDLPHSVLS/NW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

Met Pro Pro Leu Ala Ala Val Met Gly Ser Leu Pro Leu Leu Leu Cys

-25 -20 -15 -10

Met Asp Leu Pro His Ser Val Leu Ser Asn Trp

 -5 1

(2) INFORMATION FOR SEQ ID NO: 374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.5
seq EFLFLGFPSNSWP/HR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

Met Leu Gln Ile Pro Glu Arg Arg Glu Phe Leu Phe Leu Gly Phe Pro
-20 -15 -10

Ser Asn Ser Trp Pro His Arg
-5 1

(2) INFORMATION FOR SEQ ID NO: 375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.5
seq FLITLFCVVVG/FF

(xi) SEQUENCE DESCRIPTION: SEO ID NO: 375:

Met Phe Phe Val His Phe Leu Ile Thr Leu Phe Cys Cys Cys Val Val
 -15 -10 -5

Val Gly Phe Phe Gly His Asp His Ser Phe Ile Ser Gln Phe Ile Leu
 1 5 10

Val Thr Trp Ala Arg Ala Gly
 15 20

(2) INFORMATION FOR SEQ ID NO: 376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq CLLHLRCLQLYWA/AR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

Met Ala Cys Phe Gly Glu Lys Arg His Ala Lys Ser Cys Leu Leu His
 -25 -20 -15 -10

Leu Arg Cys Leu Gln Leu Tyr Trp Ala Ala Arg
 -5 1

(2) INFORMATION FOR SEQ ID NO: 377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.4
seq PLSLALQSSCCLC/LT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

```
Met Val Asp Arg Asp Glu Asn Ile Leu Leu Lys Gln Ile Tyr Ser Pro
    -25                      -20                      -15

Leu Ser Leu Ala Leu Gln Ser Ser Cys Cys Leu Cys Leu Thr Ser Cys
    -10                      -5                      1
```

(2) INFORMATION FOR SEQ ID NO: 378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq VSVSLCVCDCVRG/ST

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

```
Met Lys Val Lys Pro Pro Phe Val Ser Val Ser Leu Cys Val Cys Asp
-20                      -15                      -10                      -5

Cys Val Arg Gly Ser Thr Leu Thr Trp Asn Arg Leu Leu Arg Val Gly
    1                      5                      10
```

Gly

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq ILLTSCFYTLVSS/TF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

```

Met Ile Ser Ser Cys Gly Val Lys Tyr Leu Phe Ser His Ala Ser Leu
      -35              -30              -25

Phe Phe Met Val Gly Ser Thr Gly Ser Leu Ile Leu Leu Thr Ser Cys
      -20              -15              -10

Phe Tyr Thr Leu Val Ser Ser Thr Phe Leu Gln Lys Leu Ser Ser Leu
      -5              1              5

Leu Leu Ile Leu Phe Thr Glu Thr Ser Val Leu Met Leu Lys Thr Phe
  10              15              20              25

Val Ala Asn Ser Cys Cys Xaa Leu Trp Ser His Asn Cys Ile Asn Phe
      30              35              40

Phe Lys Lys Val Xaa Pro Ser Tyr Cys Xaa Ser Ser Leu Leu Phe Leu
      45              50              55

Ala Val Pro Arg
      60

```

(2) INFORMATION FOR SEQ ID NO: 380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq SFLCNFLVSLSL/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

```

Met Gly Gly Gly Ile Ala Glu Ser Phe Leu Cys Asn Phe Leu Val Ser
-20              -15              -10              -5

Leu Ser Leu Ser Phe Leu His Gly Arg

```

1

5

(2) INFORMATION FOR SEQ ID NO: 381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -33..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq LAYFLCCQGVIFG/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

Met	Asp	Ala	Leu	Glu	Arg	Gly	Ser	Leu	Arg	Asn	Glu	Gln	Ala	Leu	Val
			-30					-25					-20		
Ile	Tyr	Ala	Gly	Leu	Ala	Tyr	Phe	Leu	Cys	Cys	Gln	Gly	Val	Ile	Phe
		-15				-10						-5			
Gly	Ser	Leu	Pro	Ser	Asn	Ala	Gly	Ala	Gly	Pro	Leu	Gly	Trp	Ser	Ser
	1				5					10					15

(2) INFORMATION FOR SEQ ID NO: 382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3
seq SLWFLPLPTHVYT/HT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

Met Glu Tyr Leu Phe Gln Gln Pro Gly His Ser Arg Gly Glu Ala Arg
 -35 -30 -25

Ala Ala Ala Ala Ser Leu Glu Thr Leu Ser Ser Leu Trp Phe Leu Pro
 -20 -15 -10

Leu Pro Thr His Val Tyr Thr His Thr His Ala Asn
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3
seq SSMLITILSFIFA/LG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

Met Val Ser Ser Met Leu Ile Thr Ile Leu Ser Phe Ile Phe Ala Leu
 -15 -10 -5 1

Gly Tyr His Thr Ala Ser Tyr Pro Val Ser Leu His Pro Leu Ser Phe
 5 10 15

Phe Leu His
 20

(2) INFORMATION FOR SEQ ID NO: 384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.3
seq MNLVSALASSAXG/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

Met Pro Leu Phe Thr Met Asn Leu Val Ser Ala Leu Ala Ser Ser Ala
-15 -10 -5
Xaa Gly Gln Arg Gly Ala Gly Pro Ala Leu Trp His Leu Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO: 385:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -39..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.2
seq LILLHCSIRVFF/FF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

Met Ile Cys Lys His Tyr Cys Ile Lys Lys Asn Asn Leu Asp Tyr Leu
-35 -30 -25
Asn Arg Met Val Tyr Ser Ala Gln Leu Lys Leu Ile Leu Leu Leu His
-20 -15 -10
Cys Ser Ile Arg Val Phe Phe Phe Phe
-5 1

(2) INFORMATION FOR SEQ ID NO: 386:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -53..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2
seq SFLLLQLIHEDKA/IQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

Met Lys Ile Pro Val Trp His Lys Thr Cys Phe Leu Lys Ser Glu Ser
-50 -45 -40

Phe Ser Pro Asp Asn Leu Ser Val Ser Leu Pro Cys Arg Pro Ser Gln
-35 -30 -25

Val Pro Ser Gln Gly Gln Gly Lys Ser Phe Leu Leu Leu Gln Leu Ile
-20 -15 -10

His Glu Asp Lys Ala Ile Gln Asn Glu Ala Ile Phe Gln Pro Ser Leu
-5 1 5 10

Gln Leu

(2) INFORMATION FOR SEQ ID NO: 387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2
seq FGCTFVAFXPAFA/LS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

Met Gly Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala Phe Xaa Pro
-15 -10 -5

Ala Phe Ala Leu Ser Leu Ile Thr Val Ala Gly Asp Arg Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -34..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2
seq LWSSCWLA PLADG/ML

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

Met Val Gly Gly Leu Asp Pro Pro Gly Arg Arg Arg Phe Gln Lys Gly
 -30 -25 -20

Phe Asp Trp Arg Asn Leu Trp Ser Ser Cys Trp Leu Ala Pro Leu Ala
 -15 -10 -5

Asp Gly Met Leu Arg Tyr Met Gly Gln Xaa Gln Arg Xaa Ala Ser Asn
 1 5 10

Pro Glu Gly Ser Thr Leu Glu Ala Arg Pro Pro Ala Pro Xaa Ala Ser
15 20 25 30

Val Ser Pro Ser Val Xaa Xaa Pro His Arg Pro Trp Ala Ala Lys Met
 35 40 45

Glu Thr Val Ser Pro Ala Thr Ser Xaa Ile Ala Gly Gly
 50 55

(2) INFORMATION FOR SEQ ID NO: 389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.1
seq SLLVVSCFYQISG/RW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

Met Ser Lys Met Pro Val Phe Ala Ser Leu Leu Val Val Ser Cys Phe
-20 -15 -10
Tyr Gln Ile Ser Gly Arg Trp
-5 1

(2) INFORMATION FOR SEQ ID NO: 390:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.1
seq VTQLLPFSSPDSA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

Met Xaa Val Thr Gln Leu Leu Pro Phe Ser Ser Pro Asp Ser Ala Gly
-15 -10 -5 1
Pro Phe Leu Ser Pro Phe Ser
5

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -34..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1
seq SFHFLPWALGAMA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

```

Met Gly Lys Ala Trp Gln Glu Met Arg Val Glu Trp Gly Ala Asp Lys
      -30                      -25                      -20
Gly Asn Val Arg Ser Ser Phe His Phe Leu Pro Trp Ala Leu Gly Ala
      -15                      -10                      -5
Met Ala Ser Ser Glu Gln Gly Lys Glu Arg Ser Asn Leu Cys Phe Arg
      1                      5                      10
Lys Thr Pro Leu Ala Ile Thr Gly Arg Gly Ile Ala Arg Arg Pro Gly
      15                      20                      25                      30
Gly Gly Trp Met Gly Met Trp Val
                        35

```

(2) INFORMATION FOR SEQ ID NO: 392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -47..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1
seq VIRLSQFLLKCWP/RT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

```

Met Lys Val Met Met Arg Lys Arg Lys Lys Lys Asp Gln Cys Leu Pro
      -45                      -40                      -35
Gly Ile Cys Arg Ser Leu Lys Arg Arg Lys Ser Pro Arg Ser Pro Gly
      -30                      -25                      -20
Met Lys Val Ile Arg Leu Ser Gln Phe Leu Leu Lys Cys Trp Pro Arg
      -15                      -10                      -5                      1
Thr Ser Leu Thr Ala Ala Thr

```

(2) INFORMATION FOR SEQ ID NO: 393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq SFSIXTLLWGLNC/KR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

```

Met Thr Phe Ser Phe Phe Cys Phe Phe Pro Gly Phe Lys Pro Leu Leu
-35                               -30                     -25

Phe His Tyr Phe Leu Phe Xaa Ser Phe Ser Ile Xaa Thr Leu Leu Trp
-20                               -15                     -10                     -5

Gly Leu Asn Cys Lys Arg Ser Trp Asn Ile Asn Leu Arg Ile Val Xaa
      1                               5                     10

Ser Tyr Ser Ser Gly Tyr
      15

```

(2) INFORMATION FOR SEQ ID NO: 394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5

seq RLLLILSGCLVYG/TA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

Met Ala Gly Gly Met Lys Val Ala Val Ser Pro Ala Val Gly Pro Gly
 -40 -35 -30

Pro Trp Gly Ser Gly Val Gly Gly Gly Gly Thr Val Arg Leu Leu Leu
 -25 -20 -15 -10

Ile Leu Ser Gly Cys Leu Val Tyr Gly Thr Ala Glu Thr Asp Val Asn
 -5 1 5

Val Val Met Leu Gln Glu Ser Gln Val Cys Glu Lys Arg Ala Ser Leu
 10 15 20

Gly

(2) INFORMATION FOR SEQ ID NO: 395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq PLLSCSCPPPLLG/EG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

Met Val Glu Met Thr Gly Val Trp Gln Cys Gln Ala Glu Ala Val Lys
 -30 -25 -20

Gly Leu Pro Pro Leu Leu Ser Cys Ser Cys Pro Pro Pro Leu Leu Gly
 -15 -10 -5

Glu Gly His Ala Gln Ala Ser Pro Leu Ala Gln Glu Glu Asp Lys Lys
 1 5 10 15

His Thr Glu Gln Thr Gln Ala Thr Ser Pro Thr Gln Pro
 20 25

(2) INFORMATION FOR SEQ ID NO: 396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq AGLPLLLGNAPG/ES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

Met Gln Ile Thr Pro Gly Ser Ala Ala Gly Leu Leu Pro Leu Leu Leu
-20 -15 -10
Gly Asn Ala Pro Gly Glu Ser Val Gly Gly Arg Cys Xaa Pro Gly Cys
-5 1 5 10
Trp

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq TWLLLTQLQNSVFT/SF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

Met Ile Leu Ser Thr Trp Leu Leu Leu Thr Leu Gln Asn Ser Val Phe
-15 -10 -5
Thr Ser Phe Arg Ile Ser Pro Asn Arg Ile Gln Ser Met Leu Pro Pro
1 5 10 15
Met

(2) INFORMATION FOR SEQ ID NO: 398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq VCIVLALCHTSRP/MS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

Met Ala Phe His Ser Tyr Trp Gly Lys Ser Leu Gln Ser Phe Lys Thr
-30 -25 -20

Phe Met Arg Val Cys Ile Val Leu Ala Leu Cys His Thr Ser Arg Pro
-15 -10 -5

Met Ser Tyr His Val Pro Leu Ala Ala Gly Ser Pro Leu Met His Trp
1 5 10 15

Ser Pro Cys Ser Pro Val Pro Phe Ile Gly
20 25

(2) INFORMATION FOR SEQ ID NO: 399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq RFTLLPLVLHSQS/SC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

Met Lys Leu Arg Phe Thr Leu Leu Pro Leu Val Leu His Ser Gln Ser
 -15 -10 -5

Ser Cys Val Phe Trp Lys Ala Gly
 1 5

(2) INFORMATION FOR SEQ ID NO: 400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -30..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq FIPFLVIYSFVLS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

Met Met Ile Ile Leu Gly Phe Ala Phe Cys Pro Gly His Phe Arg Phe
 -30 -25 -20 -15

Asn Phe Ile Pro Phe Leu Val Ile Tyr Ser Phe Val Leu Ser Ser Pro
 -10 -5 1

His Thr His Arg Glu Pro Tyr Ser Pro Val Ala Asp Phe Asn Glu Cys
 5 10 15

Asn Arg Ser
 20

(2) INFORMATION FOR SEQ ID NO: 401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -27..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
seq CLLSYIALGAIHA/KI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met Cys Leu Ile Cys Leu
-25 -20 -15
Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala Lys Ile Cys Arg Arg
-10 -5 1 5
Ala Phe Gln Glu Glu Gly Arg Ala Xaa Ala Lys Thr Gly Val
10 15

(2) INFORMATION FOR SEQ ID NO: 402:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq LFLNLPLVIGTIP/LH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

Met Asp Leu Phe Leu Asn Leu Pro Leu Val Ile Gly Thr Ile Pro Leu
-15 -10 -5 1
His Pro Phe Gly Ser Arg Thr Ser Ser Val Ser Ser Gln Cys Ser Met
5 10 15
Asn Met Asn Trp Leu Ser Leu Ser Leu Pro Glu
20 25

(2) INFORMATION FOR SEQ ID NO: 403:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 114 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -73..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq VIRSTLVLSQCLC/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

```
Met Xaa Lys Asn His Arg Asn Lys Lys Ser Ile His Phe Pro Leu Cys
      -70                      -65                      -60

Thr Ile Pro Ser Xaa Met Xaa Lys Ser Cys Thr Leu Pro Leu Gln Arg
      -55                      -50                      -45

Thr Trp Asp Xaa Xaa Pro Ser Phe Val His Trp Xaa Gln Ala Arg Leu
      -40                      -35                      -30

Gln Ser Pro Pro Xaa Ser His Leu Val Xaa Leu Ser Val Ile Arg Ser
      -25                      -20                      -15                      -10

Thr Leu Val Leu Ser Gln Cys Leu Cys Ser Arg Xaa Pro Tyr Phe Ser
      -5                      1                      5

Ala Met Met Thr Pro Lys Cys Lys Ser Ile Xaa Ala Gly Asn Ser Gly
      10                      15                      20

Met Pro Lys Arg Asn Cys Lys Val Leu Pro Ser Ser Glu Lys Met Xaa
      25                      30                      35

Val His
      40
```

(2) INFORMATION FOR SEQ ID NO: 404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq SFIALVYSSLSFQ/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

Met Ser Phe Ile Ala Leu Val Tyr Ser Ser Leu Ser Phe Gln Lys Val
-10 -5 1
Pro Gly

(2) INFORMATION FOR SEQ ID NO: 405:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -22..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq IVLFLNSXFPIIC/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

Met Val Phe Asp Thr Leu Lys Ser Arg Ile Val Leu Phe Leu Asn Ser
-20 -15 -10
Xaa Phe Pro Ile Ile Cys Ser Arg
-5 1

(2) INFORMATION FOR SEQ ID NO: 406:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -59..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.7
 seq IFLFSILLMSLRT/FH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

```

Met Leu Glu Met Glu Met Thr Trp Leu Arg Leu Cys Asp Glu Cys Ser
      -55                      -50                      -45

Arg Trp Gly Met Ala Ser Ala Trp Gly Arg Gly Gly Lys Leu Leu Gly
      -40                      -35                      -30

Ala Gln Val Ala Leu His Pro Arg Asn Cys Ser Lys Ala Lys Ile Phe
      -25                      -20                      -15

Leu Phe Ser Ile Leu Leu Met Ser Leu Arg Thr Phe His Cys Asn Tyr
      -10                      -5                      1                      5

Phe Arg Gly Asn Gly
              10
  
```

(2) INFORMATION FOR SEQ ID NO: 407:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -17..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.7
 seq MLFFLGALCRESG/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

```

Met Asp Asp Leu Met Leu Phe Phe Leu Gly Ala Leu Cys Arg Glu Ser
      -15                      -10                      -5

Gly Val Pro Ser Leu Gly Lys Gln Glu Arg Met Arg Ala Tyr Ala Ala
      1                      5                      10                      15

Glu Met Pro Pro Leu Leu Pro Ser Pro Cys Pro Pro Pro Ser His Leu
              20                      25                      30

Pro Lys Pro Ala Ser Pro Cys Pro Tyr Pro Leu Xaa Leu Leu Thr Phe
      35                      40                      45
  
```

Pro Val Gly Val Pro His Leu Pro Gly Thr Arg Leu Gln Cys Gln Gly
 50 55 60

Leu Gly His Ser Leu Xaa Arg Ala Glu Arg Gly Val Gly Gly Gly Val
 65 70 75

Ser Pro Gly
 80

(2) INFORMATION FOR SEQ ID NO: 408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq LPTLLLLPVGAPG/KK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

Met Val Leu Gly Ala Leu Asn Leu Pro Ser Gln Glu Leu Pro Thr Leu
 -25 -20 -15 -10

Leu Leu Leu Pro Val Gly Ala Pro Gly Lys Lys Lys Gly Met Glu Gly
 -5 1 5

Lys Thr Pro Leu Asp Leu Phe Ala His Phe Gly Pro Glu Pro Gly Asp
 10 15 20

His Ser Asp Pro Leu Pro Pro Ser Ala Pro Ser Pro Thr Arg Glu Gly
 25 30 35

Ala Leu Thr Pro Pro Pro Gly
 40 45

(2) INFORMATION FOR SEQ ID NO: 409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq QTFVSFLSIPVLG/LV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

```

Met Leu Val Ser Lys Ile Gln Thr Phe Val Ser Phe Leu Ser Ile Pro
      -15                      -10                      -5
Val Leu Gly Leu Val Pro Asp His Ile Leu Gln Leu Ile Thr Glu Lys
      1                      5                      10
Glu Thr
      15

```

(2) INFORMATION FOR SEQ ID NO: 410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq LLSTGLNILGTQA/FR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

```

Met Cys Asn Pro Val Ala His Thr Phe Arg Gly Val His Glu His His
      -30                      -25                      -20
Ala Met Leu Leu Ser Thr Gly Leu Asn Ile Leu Gly Thr Gln Ala Phe
      -15                      -10                      -5                      1
Arg Tyr Glu Asp Gly Gln Leu
      5

```


(2) INFORMATION FOR SEQ ID NO: 411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq ILLWEACTGRCQA/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

Met Gln Cys Trp Ile Leu Leu Trp Glu Ala Cys Thr Gly Arg Cys Gln
-15 -10 -5
Ala Ser Leu Leu Ser Pro Trp Pro Arg Gly Gly Arg Gly Lys Leu Val
1 5 10 15
Ala Val Val Ala Ala Lys Trp Leu Ala Ala Ile Cys Gly Ile Trp Ala
20 25 30
Ile Lys Glu Met Pro Ser His Gly His Ser Leu Gln Ala Gly Ala Gly
35 40 45
Glu Gly Ala Leu Val Thr Trp Ser Leu Gln Thr Ser Phe Gly Val Lys
50 55 60
Gln Tyr Lys Trp Gly Val Val Trp His Glu Ala Asn Leu Leu Leu
65 70 75

(2) INFORMATION FOR SEQ ID NO: 412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq VLCILGCHGNLCC/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

Met Thr Gly Tyr Pro Trp Ala Asn Ser Ile Thr Thr Val Leu Cys Ile
-25 -20 -15 -10

Leu Gly Cys His Gly Asn Leu Cys Cys Glu Pro Ala Val Arg Ala Leu
 -5 1 5

Gly

(2) INFORMATION FOR SEQ ID NO: 413:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -24..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.6
seq IFTALFLXLHSA/IN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

Met Val Ser Cys Asp Val Xaa Ser Tyr Val Ile Ile Phe Thr Ala Leu
 -20 -15 -10

Phe Leu Xaa Leu His Ser Val Ala Ile Asn Glu Glu Phe
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 414:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq LFAIFLMCLKSIG/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

Met Lys Ser Phe Asp Lys Lys Leu Phe Ala Ile Phe Leu Met Cys Leu
-20 -15 -10 -5

Lys Ser Ile Gly Ser Val Val Met Pro Gln Pro
1 5

(2) INFORMATION FOR SEQ ID NO: 415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -33..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5
seq LASLFGLDQXAXG/HG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

Met Phe Gly Ala Gly Asp Glu Asp Asp Thr Asp Phe Leu Ser Pro Ser
-30 -25 -20

Gly Gly Ala Arg Leu Ala Ser Leu Phe Gly Leu Asp Gln Xaa Ala Xaa
-15 -10 -5

Gly His Gly Asn Glu Phe Phe Gln Tyr Thr Ala Pro Lys Gln Pro Lys
1 5 10 15

Lys Gly Gln Gly Thr Ala Ala Thr Gly Asn Gln Ala Xaa Pro Lys Thr
20 25 30

Ala Pro Ala Xaa Met Ser Thr Pro Thr Ile Leu Val Ala Thr Ala Val
35 40 45

His Ala Tyr Arg Tyr Thr Xaa Gly Xaa Tyr Val Lys Gln Xaa Asn Leu
50 55 60

Val Leu Gln Phe Trp
65

(2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5
seq RFLSLSAADGXDX/SX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

Met	Val	Leu	Thr	Leu	Gly	Glu	Ser	Trp	Pro	Val	Leu	Val	Gly	Arg	Arg	
			-25					-20					-15			
Phe	Leu	Ser	Leu	Ser	Ala	Ala	Asp	Gly	Xaa	Asp	Xaa	Ser	Xaa	Asp	Ser	
		-10					-5					1				
Trp	Asp	Val	Glu	Arg	Val	Ala	Glu	Trp	Pro	Trp	Leu	Ser	Gly	Thr	Ile	
5					10					15					20	
Arg	Ala	Val	Ser	His	Thr	Asp	Val	Thr	Lys	Lys	Asp	Leu	Lys			
				25					30							

(2) INFORMATION FOR SEQ ID NO: 417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN .

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -25..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.4
seq VLVGVFLSTFLYC/EC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

Met Ile Ile Val Ser Glu Leu Gly Thr Pro Thr Gly Val Leu Val Gly
-25 -20 -15 -10

Val Phe Leu Ser Thr Phe Leu Tyr Cys Glu Cys Val Lys Gly Pro
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 420:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -22..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.4
seq GFLLCPLVCGLRR/WT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

Met Asn Trp Asn Val Arg Gly Thr Arg Gly Phe Leu Leu Cys Pro Leu
-20 -15 -10

Val Cys Gly Leu Arg Arg Trp Thr Ser Pro Asp Cys Cys Leu Ile Glu
-5 1 5 10

Lys Thr His Arg Gly
15

(2) INFORMATION FOR SEQ ID NO: 421:

- ```
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -19..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.4
 seq RGLLLGLAVAAAA/VR
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

Met Leu Arg Cys Gly Gly Arg Gly Leu Leu Leu Gly Leu Ala Val Ala  
-15 -10 -5

Ala Ala Ala Val Arg  
1

(2) INFORMATION FOR SEQ ID NO: 422:

- ```
(i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 27 amino acids
      (B) TYPE: AMINO ACID
      (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
      (A) ORGANISM: Homo Sapiens
      (D) DEVELOPMENTAL STAGE: Fetal
      (F) TISSUE TYPE: kidney

(ix) FEATURE:
      (A) NAME/KEY: sig_peptide
      (B) LOCATION: -14..-1
      (C) IDENTIFICATION METHOD: Von Heijne matrix
      (D) OTHER INFORMATION:  score 4.4
                               seq ILLMIVFSIFLL/CN
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

Met Ile Leu Leu Met Ile Val Phe Ser Ile Phe Leu Leu Leu Cys Asn
-10 -5 1

Leu Thr Asp Phe Tyr Leu Phe Arg Ser Asp Gly
5 10

(2) INFORMATION FOR SEQ ID NO: 423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq SLLFIFRSILISC/FS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

Met Ser Leu Leu Phe Ile Phe Arg Ser Ile Leu Ile Ser Cys Phe Ser
 -10 -5 1

Gly Asp Phe Phe Phe Phe
 5

(2) INFORMATION FOR SEQ ID NO: 424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq SKVLIQLSQAFWA/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

Met Pro Leu Ile Ser Lys Val Leu Ile Gln Leu Ser Gln Ala Phe Trp
 -15 -10 -5

Ala Ser Pro Glu Gly Arg Asn Ser Ser Gly Ser Lys Arg Lys Gln Leu
 1 5 10 15
 Val Ala Ala Val Glu Met Arg Tyr Cys Lys Arg Gln Gln Gly
 20 25

(2) INFORMATION FOR SEQ ID NO: 425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq VLLGSTAMATSLT/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

Met Asp Thr Ser Ser Val Gly Gly Leu Glu Leu Thr Asp Gln Thr Pro
 -25 -20 -15
 Val Leu Leu Gly Ser Thr Ala Met Ala Thr Ser Leu Thr Asn Val Gly
 -10 -5 1
 Asn Ser Phe Ser Gly Pro Ala Asn Pro Leu Val Ser Arg Ser Asn Lys
 5 10 15
 Phe Gln Asn Ser Ser Val Glu Asp Asp Asp Asp Val Val Phe Ile Glu
 20 25 30 35
 Pro Val Gln Pro Pro Pro Pro Ser Val Pro Val Val Ala Asp Gln Arg
 40 45 50
 Thr Ile Thr Phe Thr Ser Ser Lys Asn Xaa Glu Leu Gln Gly Asn Asp
 55 60 65
 Ser Lys Ile Thr Pro Ser Ser Lys Glu Leu Ala Ser
 70 75

(2) INFORMATION FOR SEQ ID NO: 426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -31..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.3

seq ILLLTHVPPWILE/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

Met Asp Thr Gly Glu Ser Phe Ser Pro His Thr Ser Cys Arg Gly His
-30 -25 -20

Trp Arg Ile Leu Leu Leu Thr His Val Pro Pro Trp Ile Leu Glu Asn
-15 -10 -5 1

Pro Ser Cys His Thr Arg Pro Ala Val Asp Thr Gly Glu Ser Phe Ser
5 10 15

Pro Gln Arg
20

(2) INFORMATION FOR SEQ ID NO: 427:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -31..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.3

seq LVLLSVLKEPVSR/SI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

Met Pro Tyr Leu Asp Pro Tyr Ile Thr Gln Pro Ile Ile Gln Ile Glu
-30 -25 -20

Arg Lys Leu Val Leu Leu Ser Val Leu Lys Glu Pro Val Ser Arg Ser
-15 -10 -5 1

Ile Phe Asp Tyr Ala Leu Arg Ser Lys Asp Ile Thr Ser Leu Phe Arg
 5 10 15
 His Leu His Met Arg Gln Lys Lys Arg Asn Gly Ser Leu Pro Asp Cys
 20 25 30
 Pro Pro Pro Glu Asp Pro Ala Ile Ala Gln Leu Leu Lys Lys Leu Leu
 35 40 45
 Ser Gln Gly Met Thr Glu Glu Glu Glu Asp Lys Leu Leu Ala Leu Lys
 50 55 60 65
 Asp Phe Met Met

(2) INFORMATION FOR SEQ ID NO: 428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq VLLGSTAMATSLT/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

Met Asp Thr Ser Ser Val Gly Gly Leu Glu Leu Thr Asp Gln Thr Pro
 -25 -20 -15
 Val Leu Leu Gly Ser Thr Ala Met Ala Thr Ser Leu Thr Asn Val Gly
 -10 -5 1
 Asn Ser Phe Ser Gly Pro Ala Asn Pro Leu Val Ser
 5 10 15

(2) INFORMATION FOR SEQ ID NO: 429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -28..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.2
 seq FGLLDFVVQCCDS/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

```

Met His Val Leu Phe Asn Ile Val Thr Thr Asn Xaa Xaa Asn His Phe
      -25                      -20                      -15

Gly Leu Leu Asp Phe Val Val Gln Cys Cys Asp Ser Leu Arg Asn His
      -10                      -5                      1

Xaa Xaa Ser Phe Gln Ser Ser Tyr Leu Arg Leu Asn His Ser Xaa His
   5                      10                      15                      20

Thr Cys
  
```

(2) INFORMATION FOR SEQ ID NO: 430:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -22..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.2
 seq TAYWLSFMSWAQS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

```

Met Pro Pro Gln Ser Cys Cys Ser Lys Thr Ala Tyr Trp Leu Ser Phe
      -20                      -15                      -10

Met Ser Trp Ala Gln Ser Ser Ser Phe Gly Ser Arg Xaa Glu Ser Thr
      -5                      1                      5                      10

Ser Pro Cys Thr Asp His Cys Ser Gly Pro Arg Glu Glu Gln Leu Cys
      15                      20                      25

Ser Ser Arg Val Phe His Cys Ile Thr His Pro Asn Gly Arg Ile His
  
```

30

35

40

Arg Trp

(2) INFORMATION FOR SEQ ID NO: 431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq SCVFFHFLQGGLG/FG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

Met Ser Cys Val Phe Phe His Phe Leu Gln Gly Gly Leu Gly Phe Gly
 -10 -5 1

Ser Ala Gly Arg Cys Ala Gly Asp Arg
 5 10

(2) INFORMATION FOR SEQ ID NO: 432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq LILLPIWINMAQI/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

Met Ser Ile Ser Leu Ser Ser Leu Ile Leu Leu Pro Ile Trp Ile Asn
 -20 -15 -10 -5

Met Ala Gln Ile Gln Gln Gly Gly Pro Asp Glu Lys Glu Lys Thr Thr
 1 5 10

Ala Leu Lys Asp Leu Leu Ser Arg Ile Asp Leu Asp Glu Leu Met Lys
 15 20 25

Lys Asp Glu Pro Pro Gly
 30

(2) INFORMATION FOR SEQ ID NO: 433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -34...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq SFCNAVVLSPVFQ/EE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

Met Thr Ala Leu Asn Leu Val Ala Pro Phe Ser Asp Gly Asp Ser Gly
 -30 -25 -20

Ser Val Ser Leu Ala Ser Phe Cys Asn Ala Val Val Leu Ser Pro Val
 -15 -10 -5

Phe Gln Glu Glu Glu His Leu Leu Phe Gln Lys Arg Lys Thr Lys Thr
 1 5 10

Trp Pro Pro Arg
 15

(2) INFORMATION FOR SEQ ID NO: 434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -17..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq PVQVLGLLATCQH/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

Met Trp Ser Arg Pro Val Gln Val Leu Gly Leu Leu Ala Thr Cys Gln
-15 -10 -5
His Ala Pro Ser Pro Ser Phe Lys Gly Glu Thr Cys Thr Glu Ile Glu
1 5 10 15
Ser Val Tyr Leu Ala Pro Met
20

(2) INFORMATION FOR SEQ ID NO: 435:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -24..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq SLNQILLFLLISC/RT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

Met Arg Tyr Arg Leu Arg Ile Gln Ile Thr Thr Ser Leu Asn Gln Ile
-20 -15 -10
Leu Leu Phe Leu Leu Ile Ser Cys Arg Thr Leu Ser
-5 1

(2) INFORMATION FOR SEQ ID NO: 436:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq VLLFFCCSPLYSP/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

Met Pro Phe Phe Ser Asn Gln Pro Thr Gln Val Ser Val Leu Leu Phe
-25 -20 -15 -10
Phe Cys Cys Ser Pro Leu Tyr Ser Pro Leu Phe Leu Leu Xaa Leu Ile
-5 1 5
Pro His Gln
10

(2) INFORMATION FOR SEQ ID NO: 437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq IAVGLTCQHVSHA/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

Met Arg Val Lys Asp Pro Thr Lys Ala Leu Pro Glu Lys Ala Lys Arg
-40 -35 -30
Ser Lys Arg Pro Thr Val Pro His Asp Glu Asp Ser Ser Asp Asp Ile
-25 -20 -15
Ala Val Gly Leu Thr Cys Gln His Val Ser His Ala Ile Ser Val Asn
-10 -5 1

His Val Lys Arg Ala Ile Ala Glu Asn Leu Trp Ser Val Cys Ser Glu
 5 10 15 20
 Cys Leu Lys Glu Arg Arg Phe Tyr Asp Gly Gln Leu Val Leu Thr Ser
 25 30 35
 Asp Ile Trp Leu Cys Leu Lys Cys Gly Phe Gln Gly Cys Gly Lys Asn
 40 45 50
 Ser Glu Ser Gln His Ser Leu Lys His Phe Lys Ser Ser Arg Thr Glu
 55 60 65
 Pro Leu Arg
 70

(2) INFORMATION FOR SEQ ID NO: 438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq GTYLTSSSPCLQL/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

Met Val Ser Leu Gly Tyr Tyr Leu Ile Phe Val Leu Tyr Leu Trp Leu
 -40 -35 -30
 Cys Phe Met Gln Ile Ser Glu Glu Lys Leu Ile Glu Glu His Thr Gly
 -25 -20 -15
 Thr Tyr Leu Thr Ser Ser Ser Pro Leu Cys Gln Leu Gln Pro Pro Gly
 -10 -5 1

(2) INFORMATION FOR SEQ ID NO: 439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq VLCCLLIATPTFF/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

Met Ser Leu Thr Ser Arg Xaa Xaa Ile Met Xaa Thr Ile Lys Ile Gln
-35 -30 -25 -20

Asn Ile Ser Ile Thr Lys Val Leu Cys Cys Leu Leu Ile Ala Thr Pro
-15 -10 -5

Thr Phe Phe Leu Leu Leu Pro Ser Ser Ile Pro Arg
1 5

(2) INFORMATION FOR SEQ ID NO: 440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq AGVVSTSVAAAVA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

Met Xaa Ala Glu Ala Ala Gly Val Val Ser Thr Ser Val Ala Ala Ala
-15 -10 -5

Val Ala Ala Val Ala Ala Pro Ala Gly Ala Gly
1 5

(2) INFORMATION FOR SEQ ID NO: 441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq IMSSCLALTYTNS/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

```
Met Trp Ile Met Ser Ser Cys Leu Ala Leu Thr Tyr Thr Asn Ser Ile
-15                -10                -5                1
Ser His Ser Leu Cys Leu Glu Arg Ala Tyr Ser Leu Phe Lys Val Asp
      5                10                15
```

(2) INFORMATION FOR SEQ ID NO: 442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq SNALVLVTRGSSS/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

```
Met Pro Arg Gly Val Tyr Asn Ser Asn Ala Leu Val Leu Val Thr Arg
-20                -15                -10                -5
Gly Ser Ser Ser Leu Pro Leu Gly Leu Tyr Gly Ile Asn Cys Val Gln
      1                5                10
Val Ile Lys Leu Phe Tyr Arg Gly His Leu His Trp Glu Thr Leu Leu
      15                20                25
```

Pro Ser
30

(2) INFORMATION FOR SEQ ID NO: 443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq FLLPCVHPFSVIA/VY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

Met	Ile	Glu	Pro	Cys	Glu	Lys	Met	Lys	His	Tyr	Asp	Met	Asn	Trp	Phe	
				-40					-35						-30	
Leu	Cys	Met	Tyr	Glu	Cys	Phe	Phe	Phe	His	Leu	Leu	Glu	Thr	Glu	Phe	
			-25					-20						-15		
Leu	Leu	Pro	Cys	Val	His	Pro	Phe	Ser	Val	Ile	Ala	Val	Tyr	Val	Phe	
		-10					-5								1	

(2) INFORMATION FOR SEQ ID NO: 444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -55..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq AALCGISLSQXFP/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

Met Ala Met Trp Asn Arg Pro Cys Gln Xaa Leu Pro Gln Gln Pro Leu
-55 -50 -45 -40
Val Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr Gly Arg
-35 -30 -25
Glu Leu Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys Gly Ile
-20 -15 -10
Ser Leu Ser Gln Xaa Phe Pro Glu Pro Gly
-5 1

(2) INFORMATION FOR SEQ ID NO: 445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq CLLVSYAVDSAAG/RF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

Met Glu Gln Val Cys Leu Leu Val Ser Tyr Ala Val Asp Ser Ala Ala
-15 -10 -5
Gly Arg Phe Gly
1

(2) INFORMATION FOR SEQ ID NO: 446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq ATLRCWASTPVSG/RL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

```

Met Arg Lys Ile Ser His Cys Leu His Cys Trp Pro Glu Ser Gly Ala
   -25                      -20                      -15

Thr Leu Arg Cys Trp Ala Ser Thr Pro Val Ser Gly Arg Leu Ser Ser
   -10                      -5                      1

Met Ala Val Xaa Xaa Xaa Gly Glu Xaa Pro Pro Gln Asp Ala Phe Thr
   5                      10                      15                      20

Thr Gln Trp Leu Val Arg Asp Leu Arg Gly Lys Thr Glu Lys Glu Phe
                25                      30                      35

Lys Ala Tyr Val Ser Leu Phe Met Arg His Leu Cys Glu Pro Gly Ala
                40                      45                      50

Asp Gly Ser Glu Thr Phe Ala Asp Gly Val Pro Arg Glu Gly Leu Ser
   55                      60                      65

Arg Gln Gln Val Leu Thr Arg Ile Gly Val Met Ser Leu Val Lys Lys
   70                      75                      80

Lys Gly Gln
   85

```

(2) INFORMATION FOR SEQ ID NO: 447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq LLHPCGSITLTSS/ST

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

```

Met Cys Ile Asn Asp His Ile Ile Lys Leu Leu His Pro Cys Gly Ser

```

-20

-15

-10

Ile Thr Leu Thr Ser Ser Ser Thr Thr Arg
-5 1

(2) INFORMATION FOR SEQ ID NO: 448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq VALQCGLTIPALX/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

Met Arg Cys Arg Val Ala Leu Gln Cys Gly Leu Thr Ile Pro Ala Leu
-15 -10 -5

Xaa Leu Pro Gln Gly Asp Glu Ala Gly Asp Ala Gln Asp Leu Arg Gly
1 5 10 15

Pro Ala Gln Ala Glu Tyr Leu Tyr Ile Ile Ser Pro Ser
20 25

(2) INFORMATION FOR SEQ ID NO: 449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -93..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9

seq LTSAFLWLPRHLHI/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

Met Thr Val Arg Tyr Gly Lys Phe Leu Ser Leu Leu Lys Asp Gly Ala
 -90 -85 -80

Glu Asn Asp Leu Thr Trp Val Leu Lys His Cys Glu Arg Phe Leu Lys
 -75 -70 -65

Gln Gln Gln Thr Ser Ile Lys Ser Ser Leu Leu Cys Leu Gln Gly Asn
 -60 -55 -50

Tyr Ala Gly His Asp Trp Phe Val Ser Ser Leu Phe Met Ile Met Leu
 -45 -40 -35 -30

Gly Asp Lys Glu Lys Thr Phe Gln Phe Leu His Gln Phe Ser Arg Leu
 -25 -20 -15

Leu Thr Ser Ala Phe Leu Trp Leu Pro Arg Leu His Ile Ser Val Arg
 -10 -5 1

Leu Gln Ser Val Phe Lys Gly Gly Phe Xaa Ile Leu Arg Thr Leu Tyr
 5 10 15

Leu His Ser Xaa Gly Arg
 20 25

(2) INFORMATION FOR SEQ ID NO: 450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq FFWVVLFSAGCKV/IT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

Met Ala Phe Asp Val Ser Cys Phe Phe Trp Val Val Leu Phe Ser Ala
 -20 -15 -10 -5

Gly Cys Lys Val Ile Thr Ser Trp Asp Gln Met Cys Ile Glu Lys Glu
 1 5 10

Ala Thr

(2) INFORMATION FOR SEQ ID NO: 451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq HLSSTTSPPWTHA/AI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

Met Leu Thr Arg Leu Val Leu Ser Ala His Leu Ser Ser Thr Thr Ser
-20 -15 -10

Pro Pro Trp Thr His Ala Ala Ile Ser Trp Glu Leu Asp Asn Val Leu
-5 1 5 10

Met Pro Ser Pro Arg Ile Trp Pro Leu
15

(2) INFORMATION FOR SEQ ID NO: 452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq CVNLLLGFEFVIS/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

Met Arg Tyr Phe Gln Gly Pro Ser Pro Tyr Ser Glu Ile Glu Ile Glu
 -40 -35 -30 -25

Leu Cys Asp His Val Tyr Ser Phe Gln Gly Leu Cys Val Asn Leu Leu
 -20 -15 -10

Leu Gly Phe Glu Pro Val Ile Ser Arg Ser Arg Xaa Ser Ser Leu Ala
 -5 1 5

Val Glu Ser
 10

(2) INFORMATION FOR SEQ ID NO: 453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq LASLECYVPSTNQ/WQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

Met Xaa Xaa Lys Arg Thr His Xaa Xaa Xaa Ser Val Phe Asn Gly Leu
 -40 -35 -30

Val Tyr Ala Ala Gly Gly Arg Asn Ala Glu Gly Ser Leu Ala Ser Leu
 -25 -20 -15 -10

Glu Cys Tyr Val Pro Ser Thr Asn Gln Trp Gln Pro Lys Xaa Xaa Leu
 -5 1 5

Glu Val Ala Arg Cys Cys His Ala Ser Ala Val Ala Asp Gly Arg Val
 10 15 20

Leu Val Thr Gly Gly Leu
 25

(2) INFORMATION FOR SEQ ID NO: 454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -38..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.9
seq LLFFHLLLNDFFT/FY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

Met Phe Leu Lys Val Gln Ser Gln Ser Phe Tyr Xaa Pro Tyr Arg Asp
 -35 -30 -25

Cys Leu Asn Phe His Lys Ser Thr Tyr Leu Leu Phe Phe His Leu Leu
 -20 -15 -10

Leu Asn Asp Phe Phe Thr Phe Tyr Xaa Ala Lys
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 455:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -27..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.9
seq WIILIIYTFQCNS/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

Met Gln Pro Leu Lys Ile Ile Phe Tyr Leu Ser Val Ser Ile Trp Ile
 -25 -20 -15

Ile Leu Ile Ile Tyr Thr Phe Gln Cys Asn Ser Ser Leu Ser Ile Leu
 -10 -5 1 5

Leu Leu Glu Leu

(2) INFORMATION FOR SEQ ID NO: 456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq RVAACTAAAPLQA/HG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

Met Met Arg Thr Thr Ala Arg Val Ala Ala Cys Thr Ala Ala Ala Pro
 -15 -10 -5

Leu Gln Ala His Gly Ala Xaa Ile Gln Gln Xaa Pro Asp Xaa Leu Xaa
 1 5 10

Ser Xaa Arg Leu Ser Arg Xaa Gly Leu Ser Ala Gly Arg Leu His Gln
 15 20 25

Ser Glu Thr Glu Ala Glu Leu Glu Ala Pro Gly Arg Ala
 30 35 40

(2) INFORMATION FOR SEQ ID NO: 457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -34..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq RWASSCLHPSARS/SN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:

Met Glu Ala Ala Thr Thr Leu His Pro Gly Pro Arg Pro Ala Leu Pro
-30 -25 -20

Leu Gly Ala Arg Ala Arg Trp Ala Ser Ser Cys Leu His Pro Ser Ala
-15 -10 -5

Arg Ser Ser Asn Pro Ala Gly Lys Ser Ser Arg Thr Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO: 458:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -29..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq LCPVIFFPSNCWK/EY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

Met Gln Gly Val Arg Gly Pro Val Ser Phe Ser Trp Ser Thr Thr Met
-25 -20 -15

Leu Cys Pro Val Ile Phe Phe Pro Ser Asn Cys Trp Lys Glu Tyr Asn
-10 -5 1

Arg Thr Gln
5

(2) INFORMATION FOR SEQ ID NO: 459:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq FXLLFXXFXFFRQ/XG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

Met Xaa Xaa Phe Ser Phe Xaa Leu Leu Phe Xaa Xaa Phe Xaa Phe Phe
 -15 -10 -5

Arg Gln Xaa Gly
 1

(2) INFORMATION FOR SEQ ID NO: 460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq SVRLLFRFSVIMA/SE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

Met Leu Leu Leu Ser Glu Ala Leu Ser Glu Ser Val Arg Leu Leu Phe
 -20 -15 -10

Arg Phe Ser Val Ile Met Ala Ser Glu Lys Gln Ser Phe Gln Ile
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -17..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq SLPCTTAFPLLSS/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

Met Ala Leu Ile Ser Leu Pro Cys Thr Thr Ala Phe Pro Leu Leu Ser
-15 -10 -5

Ser Lys Val Ser Gln Leu Leu Leu Pro Leu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 462:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -37..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq RVVALPLVRATCT/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

Met Ser Glu Glu Glu Ala Ala Gln Ile Pro Arg Ser Ser Val Trp Glu
-35 -30 -25

Gln Asp Gln Gln Asn Val Val Gln Arg Val Val Ala Leu Pro Leu Val
-20 -15 -10

Arg Ala Thr Cys Thr Ala Val Cys Asp Val Tyr Ser Ala Ala Lys Asp
-5 1 5 10

Arg His Pro Leu Leu Gly Ser Ala Trp
15 20

(2) INFORMATION FOR SEQ ID NO: 463:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -72..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq LAELTVDPQGALA/IR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

```
Met Ala Ala Ala Ala Ala Ala Gly Ala Ala Ser Gly Leu Pro Gly Pro
   -70                      -65                      -60

Val Ala Gln Gly Leu Lys Glu Ala Leu Val Asp Thr Leu Thr Gly Ile
   -55                      -50                      -45

Leu Ser Pro Val Gln Glu Val Arg Ala Ala Ala Glu Glu Gln Ile Lys
   -40                      -35                      -30                      -25

Val Leu Glu Val Thr Glu Glu Phe Gly Val His Leu Ala Glu Leu Thr
          -20                      -15                      -10

Val Asp Pro Gln Gly Ala Leu Ala Ile Arg Gln Leu Ala Ser Val Ile
          -5                      1                      5

Leu Lys Gln Tyr Val Glu Thr His Trp Cys Ala Gln Ser Glu Lys Phe
   10                      15                      20

Arg
  25
```

(2) INFORMATION FOR SEQ ID NO: 464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -117..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.8
seq XXXYLNFCPVCYC/FS

seq XXXYLNFCPVCYC/FS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

[illegible]

(2) INFORMATION FOR SEQ ID NO: 465:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -13..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.7
seq MIEMLIFLDCVLS/SK

seq MIEMLI FLDCVLS/SK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

Met Ile Glu Met Leu Ile Phe Leu Asp Cys Val Leu Ser Ser Lys Asp
-10 -5 1

Thr Ile Thr Met Phe Val Lys Phe Ile Pro Ile Phe Pro Phe Pro Leu
 5 10 15
 Gln Phe Tyr Leu Pro Ser Phe Leu Leu Leu Glu
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -79..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq VIGSLLVLTMLTC/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

Met His Pro Phe Leu Ala Ala His Gly Pro Ala Phe His Lys Gly Tyr
 -75 -70 -65
 Lys His Ser Thr Ile Asn Ile Val Asp Ile Tyr Pro Met Met Cys His
 -60 -55 -50
 Ile Leu Gly Leu Lys Pro His Pro Asn Asn Gly Thr Phe Gly His Thr
 -45 -40 -35
 Lys Cys Leu Leu Val Asp Gln Trp Cys Ile Asn Leu Pro Glu Ala Ile
 -30 -25 -20
 Ala Ile Val Ile Gly Ser Leu Leu Val Leu Thr Met Leu Thr Cys Arg
 -15 -10 -5 1
 Arg

(2) INFORMATION FOR SEQ ID NO: 467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -14..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq IWPMASVATLWS/FT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

```
Met Ile Trp Pro Met Ser Ala Ser Val Ala Thr Leu Trp Ser Phe Thr
      -10                      -5                      1
Ser Tyr Ile Ser Tyr Pro Ser Arg Phe Tyr Tyr Asp Ala Trp
      5                      10                      15
```

(2) INFORMATION FOR SEQ ID NO: 468:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -31..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq LFIYLVFVECLLC/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

```
Met Gly Ile Asp Ile Phe Tyr Pro Ser His Ile Pro Asp Phe His Pro
  -30                      -25                      -20
Ile His Leu Phe Ile Tyr Leu Val Phe Val Glu Cys Leu Leu Cys Thr
  -15                      -10                      -5                      1
Arg Asn Xaa Xaa Xaa Leu Ser Xaa Phe Asn Cys Asp Asn Ala Gln Ile
      5                      10                      15
Ile Phe Thr Thr Gly Ser Ser Ser Ser Gly Gly Asn Lys Pro Phe Lys
      20                      25                      30
Ser Ser Leu Cys Thr Val His Arg Gly Gln Glu Arg Glu Arg Ile Glu
      35                      40                      45
Cys Gln Gly Asn Gly
```

50

(2) INFORMATION FOR SEQ ID NO: 469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -87..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq LILQASLKGELEA/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

```

Met Lys Glu Leu Asn Gln Lys Leu Thr Asn Lys Asn Asn Lys Ile Glu
  -85                               -80                               -75

Asp Leu Glu Gln Glu Ile Lys Ile Gln Lys Gln Lys Gln Glu Thr Leu
  -70                               -65                               -60

Gln Glu Glu Ile Thr Ser Leu Gln Ser Ser Val Gln Glu Tyr Glu Glu
-55                               -50                               -45                               -40

Lys Asn Xaa Lys Ile Lys Gln Leu Leu Val Lys Thr Lys Lys Glu Leu
          -35                               -30                               -25

Ala Asp Ser Lys Gln Ala Glu Thr Asp His Leu Ile Leu Gln Ala Ser
          -20                               -15                               -10

Leu Lys Gly Glu Leu Glu Ala Ser Gln Gln Gln Val Glu Val Tyr Lys
  -5                               1                               5

Val Arg Val Leu Leu Phe Lys Ile Lys Lys Met Phe Phe His Val Glu
  10                               15                               20                               25

Val Arg Asn Gly

```

(2) INFORMATION FOR SEQ ID NO: 470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -113..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq RLLLCILIIVCYI/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

Met Gly Asn Thr Leu Lys Glu Met Gln Asp Val Gln Gly Ala Leu Gln
-110 -105 -100
Cys Tyr Thr Arg Ala Ile Gln Ile Asn Pro Ala Phe Ala Asp Ala His
-95 -90 -85
Ser Asn Leu Ala Ser Ile His Lys Asp Ser Gly Asn Ile Pro Glu Ala
-80 -75 -70
Ile Ala Ser Tyr Arg Thr Ala Leu Lys Leu Lys Pro Asp Phe Pro Asp
-65 -60 -55 -50
Ala Tyr Cys Asn Leu Ala His Cys Leu Gln Ile Val Cys Asp Trp Thr
-45 -40 -35
Asp Tyr Asp Glu Arg Met Lys Lys Leu Val Ser Ile Val Ala Asp Gln
-30 -25 -20
Leu Glu Lys Asn Arg Leu Leu Leu Cys Ile Leu Ile Ile Val Cys Tyr
-15 -10 -5
Ile Leu Phe Leu Met
1

(2) INFORMATION FOR SEQ ID NO: 471:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -39..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq VAYAIPSIPSLFC/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

Met Leu Ile Leu Ala Asp Thr Arg Arg Val Gln Gly Gly Thr Leu Gly
 -35 -30 -25
 Leu Ile Pro Ala Val Leu Asn Arg Val His Val Ala Tyr Ala Ile Pro
 -20 -15 -10
 Ser Ile Pro Ser Leu Phe Cys Gln Arg Trp
 -5 1

(2) INFORMATION FOR SEQ ID NO: 472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq CVFLFPLISNTSS/YK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

Met Leu Val Gly Ile Tyr Phe Cys Val Phe Leu Phe Pro Leu Ile Ser
 -20 -15 -10 -5
 Asn Thr Ser Ser Tyr Lys Asn Cys His Lys Thr Leu Gln His Thr Ile
 1 5 10
 Pro Pro His Gly
 15

(2) INFORMATION FOR SEQ ID NO: 473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -42..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq LLLQGACPLIFL/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

Met Phe Leu Ala Pro Ser Leu Leu Ile Thr Lys Leu Leu Thr Gly Ser
-40 -35 -30
Glu Ser Pro Asp Gly Asn Pro Pro Ala Leu Gly Arg Pro Leu Leu Leu
-25 -20 -15
Gln Gly Ala Cys Pro Cys Leu Ile Phe Leu Arg Pro Asp Glu Asn Lys
-10 -5 1 5
Lys Glu Gly Xaa Glu Glu Lys Lys Asn His Lys Leu Pro Leu Lys Thr
10 15 20
Ser Leu Gly
25

(2) INFORMATION FOR SEQ ID NO: 474:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq SKSCLFYLQKVSG/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

Met Asp Pro Ser Ala Ser Lys Ser Cys Leu Phe Tyr Leu Gln Lys Val
-15 -10 -5
Ser Gly Ile Pro Gly Leu Leu Thr
1 5

(2) INFORMATION FOR SEQ ID NO: 475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -46..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq RWLCLQAYLASFS/LE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

Met Ser Leu Thr Ala Ser Gly Pro Arg Ala Ala Trp Glu Glu Arg Val
-45 -40 -35

Gly Gly Leu His Thr Trp Gly Ala Asn Ile Pro Thr Ala Pro Asp Ser
-30 -25 -20 -15

Gln Arg Trp Leu Cys Leu Gln Ala Tyr Leu Ala Ser Phe Ser Leu Glu
-10 -5 1

Ser Pro His Arg Ile Tyr Leu Glu Ser Pro Pro Thr Leu Leu Phe Pro
5 10 15

Pro Pro
20

(2) INFORMATION FOR SEQ ID NO: 476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq AQLASPLLPGATP/VA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

```

Met Lys Tyr Gln Met Val Ser Gly Ser Ala Gln Leu Ala Ser Pro Leu
  -20                      -15                      -10

Leu Pro Gly Ala Thr Pro Val Ala Gly Thr Ile Leu Lys Ser Leu Leu
  -5                      1                      5                      10

Leu Arg Thr Val Lys Met Met Arg Val Met
                15                      20

```

(2) INFORMATION FOR SEQ ID NO: 477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq CFWGLMYXWLLLG/SX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

```

Met Asn Gly Thr Phe Pro Gly Thr Tyr Val Tyr Leu Val Ala Tyr Gly
-35                      -30                      -25                      -20

Asp Leu Arg Ile Phe Gly Cys Phe Trp Gly Leu Met Tyr Xaa Trp Leu
  -15                      -10                      -5

Leu Leu Gly Ser Xaa Gly
  1

```

(2) INFORMATION FOR SEQ ID NO: 478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 12.7
seq ILFLLSWGPLQG/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp Ser
-20 -15 -10

Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met Glu Arg
-5 1 5 10

Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln Asp Gln Ser
15 20 25

Ser Arg His Ala Ala Glu Leu Arg Asn Phe Lys Asn Lys Met Leu Pro
30 35 40

Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala Leu Arg Thr Glu Ala
45 50 55

Xaa Thr Ile Ser Xaa Gly Val Asp Arg Leu Glu Arg Glu Val Asp Tyr
60 65 70 75

Leu

(2) INFORMATION FOR SEQ ID NO: 479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.5
seq LMLLVSSLSPVQG/VL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

Met Lys Phe Ile Ser Thr Ser Leu Leu Leu Met Leu Leu Val Ser Ser
-20 -15 -10

```

Leu Ser Pro Val Gln Gly Val Leu Glu Val Tyr Tyr Thr Ser Leu Arg
  -5          1          5          10

Cys Arg Cys Val Gln Glu Ser Ser Val Phe Ile Pro Arg Arg Phe Ile
          15          20          25

Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn Gly Cys Pro Arg Lys Glu
          30          35          40

Ile Ile Val Trp Lys Lys Asn Lys Ser Ile Val Cys Val Asp Leu Lys
      45          50          55

His Arg
    60

```

(2) INFORMATION FOR SEQ ID NO: 480:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -47..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8
seq VLELLAAVCLVRG/GH

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

Met	Asn	Tyr	Gln	Tyr	Gly	Phe	Asn	Met	Val	Met	Ser	His	Pro	His	Ala
		-45					-40					-35			
Val	Asn	Glu	Ile	Ala	Leu	Ser	Leu	Asn	Asn	Lys	Asn	Pro	Arg	Thr	Lys
	-30					-25					-20				
Ala	Leu	Val	Leu	Glu	Leu	Leu	Ala	Ala	Val	Cys	Leu	Val	Arg	Gly	Gly
-15					-10					-5					1
His	Glu	Ile	Ile	Leu	Ser	Ala	Phe	Asp	Asn	Phe	Lys	Glu	Val	Cys	Gly
			5					10					15		
Glu	Lys	Gln	Arg	Phe	Glu	Lys	Leu	Met	Glu	His	Phe	Arg	Asn	Glu	Asp
		20					25					30			
Asn	Asn	Ile	Asp	Phe	Met	Val	Ala	Ser	Met	Gln	Phe	Ile	Asn	Ile	Val
	35					40					45				
Val	His	Ser	Val	Glu	Asp	Met	Asn	Phe	Arg	Val	His	Leu	Gln	Tyr	Glu
50					55					60					65

Phe Thr Lys Leu Gly Leu Xaa Glu Tyr Leu Xaa Lys Leu Lys His Thr
 70 75 80
 Glu Ser Asp Lys Leu Gln Val Gln Ile
 85 90

(2) INFORMATION FOR SEQ ID NO: 481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.7
seq LVMCFLSYFGTFA/VE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

Met Ala Gln Ser Ile His Met Tyr Ala Ala Arg Val Gln Trp Gly Leu
 -25 -20 -15
 Val Met Cys Phe Leu Ser Tyr Phe Gly Thr Phe Ala Val Glu Phe Arg
 -10 -5 1
 His Tyr Arg Tyr Glu Ile Val Cys Ser Glu Tyr Gln Glu Asn Phe Leu
 5 10 15 20
 Ser Phe Ser Glu Ser Leu Ser Glu Ala Ser Glu Tyr Gln
 25 30

(2) INFORMATION FOR SEQ ID NO: 482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.1
seq LHLFHLIRPXOG/WX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

[illegible]

(2) INFORMATION FOR SEQ ID NO: 483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.7
seq CFSLVLLLSIWT/TR

(xi) SEQUENCE DESCRIPTION: SEO ID NO: 483:

Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr
-15 -10 -5

Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
1 5 10 15

Gln Val Ser Cys Arg Ile Met Xaa Xaa Thr Leu Val Ser Lys Lys Ala
20 25 30

Asn Gln Gln Leu Asn Phe Thr Glu Xaa Xaa Gly Gly Xaa Xaa Ala Ala
 35 40 45

Gly Thr Lys Phe Gly
 50

(2) INFORMATION FOR SEQ ID NO: 484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -33..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq MTCLSVLFGYATS/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

Met Ala Met Arg Tyr Asn Arg Leu Thr Val Leu Ala Gly Ala Met Leu
 -30 -25 -20

Ala Leu Gly Leu Met Thr Cys Leu Ser Val Leu Phe Gly Tyr Ala Thr
 -15 -10 -5

Ser His Pro Gln Gly Leu Tyr Ile
 1 5

(2) INFORMATION FOR SEQ ID NO: 485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.3
seq RQLLLPLPPFSFP/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

```

Met  Pro  Gln  Gln  Pro  Val  Glu  Gln  Gly  Ser  Pro  Leu  Leu  Arg  Gln  Leu
-25                -20                -15

Leu  Leu  Pro  Leu  Pro  Pro  Phe  Ser  Phe  Pro  Ala  Pro  Ser  Pro  Cys  Pro
-10                -5                1                5

Ser  Trp  Pro  Val  Ala  Leu  Gly  Ser  His  Gly  Val  Ala  Tyr  Trp  Gly  Ser
                10                15                20

Cys  Ser  Leu  Gly  His
                25

```

(2) INFORMATION FOR SEQ ID NO: 486:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -80..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.2
seq RASLLPMLLGSWA/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

```

Met  Pro  Ser  Arg  Ser  Pro  Phe  Thr  Trp  Ser  His  Leu  Cys  Trp  Arg  Ala
-80                -75                -70                -65

Gly  Arg  Cys  Pro  Arg  Trp  Arg  Ala  Cys  Leu  Ser  Ser  Ser  Ser  Val  Arg
                -60                -55                -50

Met  Cys  Ser  Pro  Ala  Ala  Pro  Ser  Arg  Phe  Gly  Ala  Leu  Gly  Xaa  Ser
                -45                -40                -35

Ala  Arg  Arg  Trp  Pro  Arg  Arg  Asp  Ala  Asp  Thr  Trp  Cys  Ala  Pro  Gln
                -30                -25                -20

Gly  Val  Met  Arg  Ala  Ser  Leu  Leu  Pro  Met  Leu  Leu  Gly  Ser  Trp  Ala
                -15                -10                -5

Phe  Leu  Pro  Pro  Ser  Cys  Ser  Pro  Arg  Ala
1                5                10

```

(2) INFORMATION FOR SEQ ID NO: 487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6
seq LTYGIILTHGASG/DM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

```

Met Ser His Thr Glu Val Lys Leu Lys Ile Pro Phe Gly Asn Lys Leu
-40                               -35                -30                -25

Leu Asp Ala Val Cys Leu Val Pro Asn Lys Ser Leu Thr Tyr Gly Ile
                -20                        -15                -10

Ile Leu Thr His Gly Ala Ser Gly Asp Met Asn Leu Pro His Leu Met
                -5                        1                        5

Ser Leu Ala Ser His Leu Ala Ser His Gly Phe Phe Cys Leu Arg Phe
    10                        15                        20

Thr Cys Lys Gly Leu Asn Ile Val His Arg Ile Lys Ala Tyr Lys Ser
    25                        30                        35                40

Val Leu Asn Tyr Leu Lys Thr Ser Gly Xaa Tyr Lys Leu Ala Gly
                45                        50                55

```

(2) INFORMATION FOR SEQ ID NO: 488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -40..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6
 seq LCXEFXSVASCDA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

```

Met Glu Leu Gly Ser Cys Leu Glu Gly Gly Arg Glu Ala Ala Glu Glu
-40                -35                -30                -25

Glu Gly Glu Pro Glu Val Lys Lys Arg Arg Leu Leu Cys Xaa Glu Phe
                -20                -15                -10

Xaa Ser Val Ala Ser Cys Asp Ala Ala Val Ala Gln Cys Phe Leu Ala
                -5                1                5

Xaa Asn Asp Trp Glu Met Glu Arg Ala Leu Asn Ser Tyr Phe Glu Pro
    10                15                20

Pro Val Glu Glu Ser Ala Leu Glu Arg Arg Pro Xaa
    25                30                35
  
```

(2) INFORMATION FOR SEQ ID NO: 489:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -36..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.8
 seq AFVSGLLIGQCSS/QK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

```

Met Gly Arg Thr Tyr Ile Val Glu Glu Thr Val Gly Gln Tyr Leu Ser
-35                -30                -25

Asn Ile Asn Leu Gln Gly Lys Ala Phe Val Ser Gly Leu Leu Ile Gly
-20                -15                -10                -5

Gln Cys Ser Ser Gln Lys Asp Tyr Val Ile Leu Ala Thr Arg Thr Pro
    1                5                10

Pro Lys Glu Glu Gln Ser Glu Asn Leu
    15                20
  
```

(2) INFORMATION FOR SEQ ID NO: 490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq CLSCLLIPLALWS/II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

```

Met Gly Ser Arg Lys Cys Gly Gly Cys Leu Ser Cys Leu Leu Ile Pro
-20                               -15                               -10

Leu Ala Leu Trp Ser Ile Ile Val Asn Ile Leu Leu Tyr Phe Pro Asn
-5                               1                               5                               10

Gly Gln Thr Ser Tyr Ala Ser Ser Asn Lys Leu Thr Asn Tyr Val Trp
15                               20                               25

Tyr Phe Glu Gly Ile Cys Phe Ser Gly Ile Met Met Leu Ile Val Thr
30                               35                               40

Thr Val Leu Leu Val Leu Glu Asn Asn Asn Asn Tyr Lys Cys Cys Gln
45                               50                               55

Ser Glu Asn Cys Ser Lys Lys Tyr Val Thr Leu Leu Ser Ile Ile Phe
60                               65                               70                               75

Ser Ser Leu Gly Ile Ala Phe Ser Gly Tyr Cys Leu Val Ile Ser Ala
80                               85                               90

Leu Gly Leu Val Gln Gly Pro Tyr Cys Arg
95                               100

```

(2) INFORMATION FOR SEQ ID NO: 491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -21..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.6
 seq CLSCLLIPLALWS/II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

```

Met Gly Ser Arg Lys Cys Gly Gly Cys Leu Ser Cys Leu Leu Ile Pro
-20                               -15                -10

Leu Ala Leu Trp Ser Ile Ile Val Asn Ile Leu Leu Tyr Phe Pro Asn
-5                               1                   5                10

Gly Gln Thr Ser Tyr Ala Ser Ser Asn Lys Leu Thr Asn Tyr Val Trp
15                               20                25

Tyr Phe Glu Gly Ile Cys Phe Ser Gly Ile Met Met Leu Ile Val Thr
30                               35                40

Thr Val Leu Leu Val Leu Glu Asn Asn Asn Asn Tyr Lys Cys Cys Gln
45                               50                55

Ser Glu Asn Cys Ser Lys Lys Tyr Val Thr Leu Leu Ser Ile Ile Phe
60                               65                70                75

Ser Ser Leu Gly Ile Ala Phe Ser Gly Tyr Cys Leu Val Ile Ser Ala
80                               85                90

Leu Gly Leu Val Gln Gly Pro Tyr Cys Arg Thr Leu Asp Gly Trp Glu
95                               100               105

Tyr Ala Phe Glu Gly Thr Xaa Gly Arg Phe Leu Thr Asp Ser Ser Ile
110                               115               120

Trp Ile Gln Cys Leu Glu
125

```

(2) INFORMATION FOR SEQ ID NO: 492:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq SFLPSALVIWTS/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

```

Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
-20                               -15                -10

Ile Trp Thr Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr
-5                               1                 5                10

Leu His His Ile
15

```

(2) INFORMATION FOR SEQ ID NO: 493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq PLIFSLWCSGVLL/HI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

```

Met Phe Asn Ala Ser Thr Phe Thr Asp Trp Ser Ser Ser Ile Phe Phe
-40                               -35                -30

Val Phe Thr Phe Lys Ser Lys Lys Ser Ala Gly Leu Pro Leu Ile Phe
-25                               -20                -15                -10

Ser Leu Trp Cys Ser Gly Val Leu Leu His Ile His Gln Lys Ala Gly
-5                               1                 5

Gly Pro Arg Leu Trp Arg Ile His Gly Glu Gln
10                               15

```

(2) INFORMATION FOR SEQ ID NO: 494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.4
seq SLLLVQLLTPCSA/QF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

Met Lys Met Ala Ser Ser Leu Ala Phe Leu Leu Leu Asn Phe His Val
 -25 -20 -15

Ser Leu Leu Leu Val Gln Leu Leu Thr Pro Cys Ser Ala Gln Phe Ser
 -10 -5 1

Val Leu Gly Pro Leu
 5

(2) INFORMATION FOR SEQ ID NO: 495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -42..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2
seq LLFDLVCFEFCQS/DD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

Met His Ile Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala
 -40 -35 -30

Ile Val His Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe
 -25 -20 -15

Asp Leu Val Cys His Glu Phe Cys Gln Ser Asp Asp Pro Ala Arg
 -10 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -43..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2
seq PMQLLQVLSDVLA/EI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

Met Ser Asp Gln Ile Lys Phe Ile Met Asp Ser Leu Asn Lys Glu Pro
 -40 -35 -30

Phe Arg Lys Asn Tyr Asn Leu Ile Thr Phe Xaa Ser Leu Glu Pro Met
 -25 -20 -15

Gln Leu Leu Gln Val Leu Ser Asp Val Leu Ala Glu Ile Asp Pro Lys
 -10 -5 1 5

Gln Leu Val Asp Ile Arg Glu Glu Met Pro Glu Gln Thr Ala Lys Arg
 10 15 20

Met Leu Ser Leu Leu Gly Ile Leu Lys Tyr Lys Pro Ser Gly Asn Ala
 25 30 35

Thr Asp Met Ser Thr Phe Arg Gln Gly Leu Val Ile Gly Ser Lys Pro
 40 45 50

Val Ile Tyr Pro Val Leu
 55

(2) INFORMATION FOR SEQ ID NO: 497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -79..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq IIHAXGLVRECLA/XT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

```
Met Ala Thr Ser Ser Gln Xaa Arg Gln Leu Leu Ser Asp Tyr Gly Pro
               -75                      -70                      -65

Pro Ser Leu Gly Tyr Thr Gln Gly Thr Gly Asn Ser Gln Xaa Pro Gln
               -60                      -55                      -50

Ser Lys Tyr Ala Glu Leu Leu Ala Ile Ile Xaa Glu Leu Gly Lys Glu
               -45                      -40                      -35

Ile Arg Pro Met Tyr Ala Gly Ser Lys Ser Ala Met Glu Arg Leu Lys
               -30                      -25                      -20

Arg Gly Ile Ile His Ala Xaa Gly Leu Val Arg Glu Cys Leu Ala Xaa
-15                      -10                      -5                      1

Thr Glu Arg Met Pro Asp Pro Ser Cys Leu Val Gly Phe
               5                      10
```

(2) INFORMATION FOR SEQ ID NO: 498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5
seq LLGAAAVAALGRG/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

```

Met Arg Leu Leu Gly Ala Ala Ala Val Ala Ala Leu Gly Arg Gly Arg
-15          -10          -5          1
Ala Pro Ala Ser Leu Gly Trp Gln Arg Lys Gln Val Asn Trp Lys Ala
          5          10          15
Cys Arg Trp Ser Ser Ser Gly Val Ile Pro Asn Glu Lys Ile Arg Asn
          20          25          30
Ile Gly Ile Ser Ala His Ile Asp Ser Gly Lys
          35          40

```

(2) INFORMATION FOR SEQ ID NO: 499:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
seq RLLRRFLASVIS/RK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

```
Met Ala Gln Arg Leu Leu Leu Arg Arg Phe Leu Ala Ser Val Ile Ser  
-15 -10 -5
```

```
Arg Lys Pro Ser Gln Gly Gln Trp Pro Pro Leu Thr Ser Arg Ala Leu  
1 5 10 15
```

```
Gln Thr Pro Gln Cys Ser Pro Gly Gly Leu Thr Val Thr Pro Asn Pro  
20 25 30
```

```
Ala Pro Gly  
35
```

(2) INFORMATION FOR SEQ ID NO: 500:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq LNSLSALAEAVG/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

Met Phe Arg Leu Asn Ser Leu Ser Ala Leu Ala Glu Leu Ala Val Gly
-15 -10 -5

Ser Arg Trp Tyr His Gly Gly Ser Gln Pro Ile Gln Ile Arg Leu Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -61..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq YTAVSVLAGPRWA/DP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

Met Ser Gly Ser Asn Gly Ser Lys Glu Asn Ser His Asn Lys Ala Arg
-60 -55 -50

Thr Ser Pro Tyr Pro Gly Ser Lys Val Glu Arg Ser Gln Val Pro Asn
-45 -40 -35 -30

Glu Lys Val Gly Trp Leu Val Glu Trp Gln Asp Tyr Lys Pro Val Glu
-25 -20 -15

Tyr Thr Ala Val Ser Val Leu Ala Gly Pro Arg Trp Ala Asp Pro Gln
-10 -5 1

Ile Ser Glu Ser Asn Phe Ser Pro Lys Phe Asn Glu Lys Asp Gly His
5 10 15

Val Glu Arg Lys Ser Lys Asn Gly Leu Tyr
20 25

(2) INFORMATION FOR SEQ ID NO: 502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq TLMFSLTAQWXTS/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

Met Arg Thr Thr Leu Met Phe Ser Leu Thr Ala Gln Trp Xaa Thr Ser
-15 -10 -5

Arg Ser Ser Phe Gln
1 5

(2) INFORMATION FOR SEQ ID NO: 503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 14.1
seq LLLLLLLTLLAFA/GY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

Met Ser Asp Leu Leu Leu Leu Gly Leu Ile Gly Gly Leu Thr Leu Leu
 -25 -20 -15 -10

Leu Leu Leu Thr Leu Leu Ala Phe Ala Gly Tyr Ser Gly Leu Leu Ala
 -5 1 5

Gly Val Glu Val Ser Ala Gly Ser Pro Pro Ile Arg Asn Val Thr Val
 10 15 20

Ala Tyr Lys Phe His Met Gly Leu Tyr Gly Glu Thr Gly Arg Leu Phe
 25 30 35

Thr Glu Ser Cys Ser Ile Ser Pro Lys Leu Arg Ser Ile Ala Val Tyr
 40 45 50 55

Tyr Asp Asn Pro His Met Val Pro Pro Asp Lys Cys Arg Cys Ala Val
 60 65 70

Gly Ser Ile Leu Ser Glu Gly Glu
 75

(2) INFORMATION FOR SEQ ID NO: 504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.4
seq LWSLALWLPLALS/VS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

Met Glu Gly Thr Glu Met Gly Ala Arg Pro Gly Gly His Pro Xaa Lys
 -30 -25 -20

Trp Ser Phe Leu Trp Ser Leu Ala Leu Trp Leu Pro Leu Ala Leu Ser
 -15 -10 -5

Val Ser Leu Phe Leu Gly Leu Ser Leu Ser Pro Pro Gln Pro Gly Leu
 1 5 10 15

Ser Leu Trp Cys Thr Leu Ser Tyr Cys Cys Glu Gln Trp Lys Phe Lys
 20 25 30

Gly Thr Pro Ser Pro Ala Leu Leu Asn Leu Gly Thr Arg Gly
 35 40 45

(2) INFORMATION FOR SEQ ID NO: 505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -55..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.2
seq LLFALGSLGLIFA/LI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

Met Xaa Phe Leu Arg Lys Val Xaa Ser Ile Leu Ser Leu Gln Val Leu
-55 -50 -45 -40

Leu Thr Thr Val Thr Ser Thr Val Phe Leu Tyr Phe Glu Ser Val Arg
-35 -30 -25

Thr Phe Val Xaa Glu Ser Pro Ala Leu Ile Leu Leu Phe Ala Leu Gly
-20 -15 -10

Ser Leu Gly Leu Ile Phe Ala Leu Ile Leu Asn Xaa His Lys Tyr Pro
-5 1 5

Leu Asn Leu Tyr Leu Leu Phe Gly Phe Thr Leu Leu Xaa Ala Leu Thr
10 15 20 25

Val Ala Val Val Val Thr
30

(2) INFORMATION FOR SEQ ID NO: 506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: -38..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: - score 10.8
seq MLLLLLLLGSGQG/PQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

Met Ala Ala Thr Leu Gly Pro Leu Gly Ser Trp Gln Gln Trp Arg Arg
-35 -30 -25

Cys Leu Ser Ala Arg Asp Gly Ser Arg Met Leu Leu Leu Leu Leu Leu
-20 -15 -10

Leu Gly Ser Gly Gln Gly Pro Gln Gln Val Gly Ala Gly
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 507:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

```
(ix) FEATURE:
      (A) NAME/KEY: sig_peptide
      (B) LOCATION: -41..-1
      (C) IDENTIFICATION METHOD: Von Heijne matrix
      (D) OTHER INFORMATION:  score 9.9
                               seq ILPFLLPFPVNA/RS
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507:

[illegible]

(2) INFORMATION FOR SEQ ID NO: 508:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.7
seq QLCLLLLPSCLS/VS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

Met Ala Pro Gly Val Ile Ile Ile Gln Leu Cys Leu Leu Leu Leu Pro
-20 -15 -10

Ser Cys Ser Leu Ser Val Ser Gly Cys Ser Cys Pro Ser Ala Cys Phe
-5 1 5 10

Ser Thr Thr Ser Arg Glu
15

(2) INFORMATION FOR SEQ ID NO: 509:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -93..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.6
seq LSLSLGASAPVQC/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

Met Arg His Gly Phe Ile Gln Gln Gln Phe Ser Leu Thr Ala Phe Ser
-90 -85 -80

Xaa Xaa Xaa Xaa Ile Phe Thr Leu Xaa Xaa Leu Ser Gln Leu Leu Ser
-75 -70 -65

Ser Ala Ala Pro Lys His Thr Ala Ala Pro Thr Ala Leu Pro Cys Leu

-60

-55

-50

Gln Gly Gln Gln Leu Asn Ser Leu Ser Leu Gly Thr Ser Glu Leu Ser
 -45 -40 -35 -30

Cys Val Leu Ala Ser Ser Cys Leu Ser Thr Lys Thr Asp Pro Ser Gly
 -25 -20 -15

Leu Ser Leu Ser Leu Gly Ala Ser Ala Pro Val Gln Cys Gln Gln Asp
 -10 -5 1

Asn Tyr Thr Phe Cys Xaa Gln Tyr Trp Leu Arg Ala Arg His
 5 10 15

(2) INFORMATION FOR SEQ ID NO: 510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.5
seq LIIFLSFLPFINS/SF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

Met Phe Gln Asn Ile Gln Lys Cys Leu Asn Val Pro Phe Val Arg Gly
 -40 -35 -30

Tyr His Val Phe Tyr Ile Asn Leu Asn Ala Val Ile Leu Ile Ile Phe
 -25 -20 -15 -10

Leu Ser Phe Leu Pro Phe Ile Asn Ser Ser Phe Val Tyr Lys Thr Asn
 -5 1 5

Pro Leu Tyr Asp Ala Ile Ser Asn Tyr Val Phe Ser Phe Arg Tyr Pro
 10 15 20

Asn Leu Xaa Xaa Phe Ala Leu Asp Val Arg Leu Val Phe
 25 30 35

(2) INFORMATION FOR SEQ ID NO: 511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -20..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.2
seq FPVLALFLSGSLA/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

Met Ser Leu Ser Gln Arg Gly Phe Pro Val Leu Ala Leu Phe Leu Ser
-20 -15 -10 -5

Gly Ser Leu Ala Leu Phe His His Thr Ser Gly
1 5

(2) INFORMATION FOR SEQ ID NO: 512:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -29..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.9
seq ALLIVCDVPSASA/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val Val
-25 -20 -15

Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln Arg Lys
-10 -5 1

Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met Glu Trp Thr
5 10 15

Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys Phe Arg Arg Leu
 20 25 30 35
 Val Lys Xaa Pro Pro Arg
 40

(2) INFORMATION FOR SEQ ID NO: 513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8
seq VPMLLLIVGGSFG/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu
 -30 -25 -20
 Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly
 -15 -10 -5
 Leu Arg Glu Phe Ser Xaa Ile Arg Tyr Asp Ala Val Lys Gly
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.5

seq LLVLLLYAPVGFC/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

Met Glu Leu Pro Ser Gly Pro Gly Pro Glu Arg Leu Phe Asp Ser His
-35 -30 -25

Arg Leu Pro Gly Asp Cys Phe Leu Leu Leu Val Leu Leu Leu Tyr Ala
-20 -15 -10

Pro Val Gly Phe Cys Leu Leu Val Leu Xaa Leu Phe Leu Gly Ile His
-5 1 5 10

Val Phe Leu Val Ser Cys Ala Leu Pro Asp Ser Val Leu Arg Arg Phe
15 20 25

Val Val Arg Thr Met Cys Ala Val Leu Gly Leu Val Ala Arg Gln Glu
30 35 40

Asp Ser Gly Leu Arg Asp His Ser Val Arg Val Leu Ile Ser Asn His
45 50 55

Val Thr Pro Phe Asp His Gln
60 65

(2) INFORMATION FOR SEQ ID NO: 515:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig peptide

(B) LOCATION: -90..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 8.4
seq SLVLLTVTPSXRQ/QE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

Met Ala Gln Ser Gln Gly Trp Val Xaa Arg Tyr Xaa Lys Ala Phe Cys
-90 -85 -80 -75

Lys Gly Phe Phe Val Ala Val Pro Val Ala Val Thr Phe Leu Asp Arg
-70 -65 -60

Val Ala Cys Val Ala Arg Val Glu Gly Ala Ser Met Gln Pro Ser Leu
-55 -50 -45

Asn Pro Gly Gly Ser Xaa Ser Ser Asp Val Val Xaa Xaa Asn His Trp
-40 -35 -30

Lys Val Arg Asn Phe Glu Val His Arg Gly Asp Ile Val Ser Leu Val
-25 -20 -15

Leu Leu Thr Val Thr Pro Ser Xaa Arg Gln Gln Glu
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -23..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.1
seq WLLVLSFVFGCNV/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

Met Ser Ser Ala Ala Asp His Trp Ala Trp Leu Leu Val Leu Ser
-20 -15 -10

Phe Val Phe Gly Cys Asn Val Leu Arg Ile Leu Xaa Pro Xaa Xaa Xaa
-5 1 5

Ile Xaa Xaa Val Gln Gly Ala Ala Glu Gly Arg Gly Xaa Glu Ser Gln
10 15 20 25

Met Arg Ala Glu Ile Gln Asp Met Lys Gln Glu Leu Ser Thr Val Asn
30 35 40

Met Met Asp Glu Phe Ala Arg Tyr Ala Arg Leu Xaa Arg Lys Ile Asn
45 50 55

Lys Met Thr Asp Lys
60

(2) INFORMATION FOR SEQ ID NO: 517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -20..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8
seq HVFFLLLLAHIIA/LE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

Met Asn Leu Phe Lys Thr Asn His Val Phe Phe Leu Leu Leu Leu Ala
-20 -15 -10 -5

His Ile Ile Ala Leu Glu Ser Ile Ala Trp Phe Thr Val Phe Tyr Phe
1 5 10

Gly Asn

(2) INFORMATION FOR SEQ ID NO: 518:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -24..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.9
seq LLLPRVLLTMASG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

Met Pro Ala Leu Leu Pro Val Ala Ser Arg Leu Leu Leu Leu Pro Arg
-20 -15 -10

Val Leu Leu Thr Met Ala Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro
-5 1 5

Ala Ser Asp Ser Gly Ser Gly Tyr Val Pro Gly
10 15

(2) INFORMATION FOR SEQ ID NO: 519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -66..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9
seq LLLPRVLLTMASG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

Met Ile Gly Ser Gly Leu Ala Gly Ser Gly Gly Ala Gly Gly Pro Ser
-65 -60 -55

Ser Thr Val Thr Trp Cys Ala Leu Phe Ser Asn His Val Ala Ala Thr
-50 -45 -40 -35

Gln Ala Ser Leu Leu Leu Ser Phe Val Trp Met Pro Ala Leu Leu Pro
-30 -25 -20

Val Ala Ser Arg Leu Leu Leu Leu Pro Arg Val Leu Leu Thr Met Ala
-15 -10 -5

Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro Ala Ser Asp Ser Gly Ser
1 5 10

Gly Tyr Val Pro Gly Ser Val Ser Ala Ala Phe Val Thr Cys Pro Arg
15 20 25 30

(2) INFORMATION FOR SEQ ID NO: 520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: -24..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.9
 seq LLLPRVLLTMASG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

```

Met Pro Ala Leu Leu Pro Val Ala Ser Arg Leu Leu Leu Leu Pro Arg
      -20                      -15                      -10

Val Leu Leu Thr Met Ala Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro
      -5                      1                      5

Ala Ser Asp Ser Gly Ser Gly Tyr Val Pro Gly Ser Val Ser Ala Ala
      10                      15                      20

Phe Val Thr Cys Pro Asn Glu Lys Val Ala Lys Glu Ile Ala Arg Ala
      25                      30                      35                      40

Val Val Glu Lys Arg Leu Ala Ala Cys Val Asn Leu Ile Pro Gln Ile
      45                      50                      55

Thr Ser Ile Tyr Glu Trp Lys Gly Xaa Ile Glu Glu Asp Ser Glu Val
      60                      65                      70

Leu Met Met Ile Lys Thr Gln Ala
      75                      80
  
```

(2) INFORMATION FOR SEQ ID NO: 521:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -92..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.6
 seq FLLLTVALLASYS/VH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

```

Met Glu Ala Ser Trp Gly Ser Phe Asn Ala Glu Arg Gly Trp Tyr Val
      -90                      -85                      -80

Ser Val Gln Gln Pro Glu Glu Ala Glu Ala Glu Glu Leu Ser Pro Leu
      -75                      -70                      -65
  
```

Leu Ser Asn Glu Leu His Arg Gln Arg Ser Pro Gly Val Ser Phe Gly
 -60 -55 -50 -45
 Leu Ser Val Phe Asn Leu Met Asn Ala Ile Met Gly Ser Gly Ile Leu
 -40 -35 -30
 Gly Leu Ala Tyr Val Met Ala Asn Thr Gly Val Phe Gly Phe Ser Phe
 -25 -20 -15
 Leu Leu Leu Thr Val Ala Leu Leu Ala Ser Tyr Ser Val His Leu Leu
 -10 -5 1
 Leu Ser Met Cys Ile Gln Thr Ala Val Thr Ser Tyr Glu Asp Leu Gly
 5 10 15 20
 Leu Phe Ala Phe Gly Leu Pro Gly Leu
 25

(2) INFORMATION FOR SEQ ID NO: 522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6
seq FFLLLRFFLRIDG/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

Met Pro Ser Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp
 -15 -10 -5
 Gly Val Pro
 1

(2) INFORMATION FOR SEQ ID NO: 523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -19..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.6
 seq FIVGIYFLSSCRA/EE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

```

Met Lys Arg Thr His Leu Phe Ile Val Gly Ile Tyr Phe Leu Ser Ser
      -15                      -10                      -5

Cys Arg Ala Glu Glu Gly Leu Asn Phe Pro Thr Tyr Asp Gly Lys Asp
      1                      5                      10

Arg Val Val Ser Leu Ser Glu Lys Asn Phe Lys Gln Val Leu
      15                      20                      25
  
```

(2) INFORMATION FOR SEQ ID NO: 524:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -23..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.4
 seq VLLLAALPPVLLP/GA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

```

Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Ala Ala
      -20                      -15                      -10

Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
      -5                      1                      5

Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
      10                      15                      20                      25

Tyr Gln Pro Met Pro Leu Xaa Ala Ser Leu Glu Ile Glu
      30                      35
  
```


(2) INFORMATION FOR SEQ ID NO: 525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.3
seq LLSACLVTLWGLG/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
-35 -30 -25

Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
-20 -15 -10

Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
-5 1 5 10

Leu Xaa Leu Ala Ser Leu Gln Leu Gly
15 20

(2) INFORMATION FOR SEQ ID NO: 526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.3
seq HLLLLLLLPAPTLK/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

Met Gly Ala Trp Gly Arg Gly Trp Pro Trp Glu Glu Arg Gln Gly His
 -25 -20 -15

His Leu Leu Leu Leu Leu Leu Pro Ala Pro Thr Leu Lys Gly Leu Gly
 -10 -5 1

Ala Ala Gln Leu Pro Leu Cys Pro Ser Gly Gly Leu Ser Pro Leu Leu
 5 10 15

Thr Leu Leu Gln Ser Gly
 20 25

(2) INFORMATION FOR SEQ ID NO: 527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -75..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2
seq LLFIIGLIGCCAT/IR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527:

Met Gly Gln Cys Gly Ile Thr Ser Ser Lys Thr Val Leu Val Phe Leu
 -75 -70 -65 -60

Asn Leu Ile Phe Trp Gly Ala Ala Gly Ile Leu Cys Tyr Val Gly Ala
 -55 -50 -45

Tyr Val Phe Ile Thr Tyr Asp Asp Tyr Asp His Phe Phe Glu Asp Val
 -40 -35 -30

Tyr Thr Leu Ile Pro Ala Val Val Ile Ile Ala Val Arg Ala Leu Leu
 -25 -20 -15

Phe Ile Ile Gly Leu Ile Gly Cys Cys Ala Thr Ile Arg Glu Ser Arg
 -10 -5 1 5

Cys Gly Leu Ala Thr Phe Val Ile Ile Leu Leu Leu Val Phe Val Thr
 10 15 20

Glu Val Val Val Val Val Leu Gly Tyr Val Tyr Arg Ala Lys Val Glu
 25 30 35

Asn Glu Val Asp Arg Ser Ile Gln Lys Val Tyr Lys
 40 45

(2) INFORMATION FOR SEQ ID NO: 528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -65..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq IGHFLCLVILVYC/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

```

Met Pro Xaa Ala Phe Ser Val Ser Ser Phe Pro Val Ser Ile Pro Ala
-65                               -60                     -55           -50

Val Leu Thr Gln Thr Asp Trp Thr Glu Pro Trp Leu Met Gly Leu Ala
                               -45                     -40           -35

Thr Phe His Ala Leu Cys Val Leu Leu Thr Cys Leu Ser Ser Arg Ser
          -30                               -25                     -20

Tyr Arg Leu Gln Ile Gly His Phe Leu Cys Leu Val Ile Leu Val Tyr
          -15                               -10                     -5

Cys Ala Glu Tyr Ile Asn Glu Ala Ala Ala Met Asn Trp Arg Leu Phe
   1                               5                     10           15

Ser Xaa Tyr Gln Tyr Phe Asp Ser Arg Gly Met Phe Ile Ser Ile Val
          20                               25                     30

Phe Ser Ala Pro Leu Leu Val Asn Ala Met Ile Ile Val Val Met Trp
          35                               40                     45

Val Trp Lys
          50

```

(2) INFORMATION FOR SEQ ID NO: 529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq LLLSLFFPLRISL/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

```

Met Leu Leu Leu Ser Leu Phe Phe Pro Leu Arg Ile Ser Leu Ser Pro
      -10                      -5                      1
Ser Asn His Leu Trp Ser Ala Ser Ser Gly
      5                      10

```

(2) INFORMATION FOR SEQ ID NO: 530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6
seq LILVLQLLLRIRR/NR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

```

Met Glu Thr Gly Glu Arg Ala Arg Leu Ile Leu Ile Leu Val Leu Gln
      -20                      -15                      -10
Leu Leu Leu Arg Ile Arg Arg Asn Arg Gln Gln Arg Cys Xaa Ala Ser
      -5                      1                      5
Ser Ala Thr Ala Pro Ser Ser His Gly Cys Asp Leu Arg Gly Gly Lys
      10                      15                      20                      25
Leu Asn Phe Lys Thr Thr Pro Met Asp Ala Asp Ser Asp Val Ala Leu
      30                      35                      40
Asp Ile Leu Ile Thr Asn Val Val Cys Val Phe Arg Thr Arg Cys Arg

```

45

50

55

(2) INFORMATION FOR SEQ ID NO: 531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.4
seq ILGCSSVCQLCTG/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

Met Cys Gly Xaa Xaa Phe Ser Leu Pro Cys Leu Arg Leu Phe Leu Val
-40 -35 -30

Val Thr Cys Tyr Xaa Leu Leu Leu His Lys Glu Ile Leu Gly Cys
-25 -20 -15 -10

Ser Ser Val Cys Gln Leu Cys Thr Gly Arg Gln Ile Asn Cys Arg Asn
-5 1 5

Leu Gly Leu Ser Ser Ile Leu Arg Ile Phe Leu Lys Val Gln Phe Phe
10 15 20

Cys Ile
25

(2) INFORMATION FOR SEQ ID NO: 532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: -73..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.4
 seq ACCFLSAFSPTLT/KS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

```

Met Asn Pro Val Thr Glu Ser Pro Ser Cys Leu Phe Ser Pro Pro Ser
      -70                      -65                      -60

Glu Ser Ala Leu Ala Ser Gln Leu Ala Leu Ser Ala Ser Cys Asp Gln
      -55                      -50                      -45

Arg Ala Pro Phe Ser Leu Ala Gly Val Xaa Ser Xaa Xaa Pro Arg Leu
      -40                      -35                      -30

Ala Ser Arg Gln Val Ala Pro Pro Phe Gly Ser Arg Ala Cys Cys Phe
      -25                      -20                      -15                      -10

Leu Ser Ala Phe Ser Pro Thr Leu Thr Lys Ser Ala Ala Ala Thr Ser
              -5                      1                      5

Thr Ala His Thr Phe Leu Ala Asn Gln Leu Ser Cys Leu Phe Thr Lys
      10                      15                      20

Cys Leu His Asn Asn Tyr Ser Ser Ser Leu Arg Leu Thr Lys Lys Gln
      25                      30                      35

Glu Lys Ser Thr Thr Pro Gln
      40                      45
  
```

(2) INFORMATION FOR SEQ ID NO: 533:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -21..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.3
 seq LGLSVLLTAATVA/GV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

```

Met Ser Arg Ser Ser Lys Val Val Leu Gly Leu Ser Val Leu Leu Thr
      -20                      -15                      -10

Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp
  
```

-5

1

5

(2) INFORMATION FOR SEQ ID NO: 534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq GVGLVTLLGLAVG/SY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly
-25 -20 -15

Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg
-10 -5 1 5

Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Ser Glu Lys Tyr Leu
10 15 20

Leu Arg Leu Leu Asp Lys Thr Thr Pro Gly
25 30

(2) INFORMATION FOR SEQ ID NO: 535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -51..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2
seq VLLLSSAXLVXXS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

```

Met Tyr Pro Ser Tyr Leu Leu Ile Xaa Pro Pro Ile Pro Ser Gln Phe
-50                               -45                               -40

Leu Lys Gln Cys Xaa Pro Pro Thr Leu Ser Asp Pro Phe Leu Pro Leu
-35                               -30                               -25                               -20

Ala Leu Arg Ser Leu Asp Val Leu Leu Leu Ser Ser Ala Xaa Leu Val
                               -15                               -10                               -5

Xaa Xaa Ser Ser Pro Leu Glu Phe Ile Arg
                1                5

```

(2) INFORMATION FOR SEQ ID NO: 536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -33..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2
seq ILLLXTFQTWCLR/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:

```

Met Glu Gln Lys His Arg Xaa Glu Leu Glu Gln Leu Lys Leu Xaa Thr
-30                               -25                               -20

Lys Glu Asn Lys Ile Leu Leu Leu Xaa Thr Phe Gln Thr Trp Cys Leu
-15                               -10                               -5

Arg Ile Ser His Leu Gly Tyr Gln Lys His Xaa Arg Xaa Gly Cys Leu
    1                5                10                15

Asp Xaa Arg Ser Ser Leu Cys Cys Pro Trp
                20                25

```

(2) INFORMATION FOR SEQ ID NO: 537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq TLKFLTLLQKSNA/KR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

```
Met Met Thr Ala Pro Val Leu Ala Ala Gln Thr Leu Lys Phe Leu Thr
      -20                -15                -10
Leu Leu Gln Lys Ser Asn Ala Lys Arg Xaa Asn Leu Asp Arg Leu His
      -5                1                5
Asp Glu Leu Trp Tyr Asn Asp Pro Gly Gln Met Asn Asp Gly Pro Leu
  10                15                20                25
Cys Lys Cys Ser Ala Lys Ala Arg Arg Thr Gly Ile Arg His Ser Ile
      30                35                40
Tyr Pro Gly Glu Glu Ala Ile Lys Pro Cys Arg Pro Met Thr Asn Asn
      45                50                55
Ala Gly Arg Leu Phe His Tyr Arg Ile Thr Val Ser Pro Pro Thr Asn
      60                65                70
Phe Leu Thr Asp Arg Pro Thr Val Ile Glu Tyr Asp Asp His Glu Tyr
      75                80                85
Ile Phe Glu
  90
```

(2) INFORMATION FOR SEQ ID NO: 538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.9
seq ALALAXAPDLAQA/PL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

```

Met Asp Ser Ala Ala Cys Ala Ala Ala Thr Pro Val Pro Ala Leu
  -25                      -20                      -15

Ala Leu Ala Xaa Ala Pro Asp Leu Ala Gln Ala Pro Leu Ala Leu Pro
  -10                      -5                      1                      5

Gly Leu Leu Ser Pro Ser Cys Leu Leu Ser Ser Gly Gln Glu Val Asn
                      10                      15                      20

Gly Ser Glu Arg Gly Thr Cys Leu Trp Arg Pro Trp Leu Ser Ser Thr
                      25                      30                      35

Asn Asp Ser Pro Arg Gln Met Arg Lys Leu Val Asp Leu Ala Ala Gly
  40                      45                      50

Gly Ala Thr Ala Ala Glu Val Thr Lys Ala Glu Ser Xaa Xaa His His
  55                      60                      65

Pro Val Arg Leu Phe Trp
  70                      75

```

(2) INFORMATION FOR SEQ ID NO: 539:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -24..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.7
 seq ILGLLGLLGTLVA/ML

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

```

Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu
  -20                      -15                      -10

Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp Lys Thr
  -5                      1                      5

Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys

```

10 15 20
 Gly Leu Trp Met Glu Cys Ala Thr Xaa Ser Thr Gly Ile Thr Gln Cys
 25 30 35 40
 Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala Asp Ile Gln Ala Ala
 45 50 55
 Gln Ala Met Met Val Thr Ser Ser Ala Ile Ser Ser Leu Ala Cys Ile
 60 65 70
 Ile Ser Val Val Gly Met Arg Cys Thr Val Phe Cys Gln Glu Ser Arg
 75 80 85
 Ala Arg
 90

(2) INFORMATION FOR SEQ ID NO: 540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq ILGLLGLLGTLVA/ML

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu
 -20 -15 -10
 Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp Lys Thr
 -5 1 5
 Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys
 10 15 20
 Gly Leu Trp Met Glu Cys Ala
 25 30

(2) INFORMATION FOR SEQ ID NO: 541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq LLCECLLLVAGYA/HD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

Met Leu Cys Ser Leu Leu Leu Cys Glu Cys Leu Leu Leu Val Ala Gly
-15 -10 -5

Tyr Ala His Asp Asp Asp Trp Ile Asp Pro Thr Asp Met Leu Asn Tyr
1 5 10

Asp Ala Ala Ser Gly Thr Met Arg Lys Ser
15 20

(2) INFORMATION FOR SEQ ID NO: 542:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -22..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.5
seq LWYVCPCPSGAWM/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

Met Ala Ser Arg Leu Cys Gly Gly Ala Leu Trp Tyr Val Cys Pro Cys
-20 -15 -10

Pro Ser Gly Ala Trp Met Val Pro Gly
-5 1

(2) INFORMATION FOR SEQ ID NO: 543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq LGYLVLSEGAFLA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

Met Thr Ser Ala Leu Thr Gln Gly Leu Glu Arg Ile Pro Asp Gln Leu
 -25 -20 -15

Gly Tyr Leu Val Leu Ser Glu Gly Ala Val Leu Ala Ser Ser Gly Asp
 -10 -5 1

Leu Glu Asn Asp Glu Gln Ala Xaa Ser Ala Ile Ser Glu Leu Val Ser
 5 10 15 20

Thr Ala Cys Gly Phe Arg Leu His Arg Gly Met Asn Val Pro Arg
 25 30 35

(2) INFORMATION FOR SEQ ID NO: 544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -42..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq ITGVILLAVGIWG/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

```

Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys
    -40                      -35                      -30

Phe Lys Ser Val Leu Leu Ile Xaa Thr Xaa Ile Xaa Trp Ile Thr Gly
    -25                      -20                      -15

Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn
   -10                      -5                      1                      5

Tyr Phe Xaa Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Xaa Leu
      10                      15                      20

Ile Ala Thr Gly Thr Val Xaa Ile Leu Leu Gly Tyr Arg
      25                      30                      35

```

(2) INFORMATION FOR SEQ ID NO: 545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3
seq VLLGSGLTILSQP/LM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

```

Met Ala Asp Ala Ala Ser Gln Val Leu Leu Gly Ser Gly Leu Thr Ile
   -20                      -15                      -10                      -5

Leu Ser Gln Pro Leu Met Tyr Val Lys Val Leu Ile Gln Val Gly Tyr
      1                      5                      10

Glu Pro Leu Pro Pro Thr Ile Gly Arg Asn Ile Phe Gly Arg Gln Val
      15                      20                      25

Xaa Xaa Leu Pro Xaa Leu Phe Ser Tyr Ala Gln His Gly
      30                      35                      40

```

(2) INFORMATION FOR SEQ ID NO: 546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -20..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.3
seq ALIFGGFISLIGA/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546:

Met Ser Arg Asn Leu Arg Thr Ala Leu Ile Phe Gly Gly Phe Ile Ser
-20 -15 -10 -5

Leu Ile Gly Ala Ala Phe Tyr Pro Ile Tyr Phe Arg Pro His Gly
1 5 10

✓ (2) INFORMATION FOR SEQ ID NO: 547:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -17..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.1
seq LWCFHLVVLSLYS/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547:

Met Pro His Gly Leu Trp Cys Phe His Leu Val Val Leu Ser Leu Tyr
-15 -10 -5

Ser Ser Val Ala Thr Ala Arg
1 5

(2) INFORMATION FOR SEQ ID NO: 548:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -14..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5
 seq SLVAVFLSCGLIS/KN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548:

Met Ser Leu Val Ala Val Phe Leu Ser Cys Gly Leu Ile Ser Lys Asn
 -10 -5 1

His Met Leu Leu Asn Leu Pro Gly Ile Leu Ile Pro His Asn Ala Asn
 5 10 15

His Leu Leu
 20

(2) INFORMATION FOR SEQ ID NO: 549:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Kidney
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -24..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5
 seq GALAVGAVPVVLS/AM
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549:

Met Met Lys Arg Ala Ala Ala Ala Ala Val Gly Gly Ala Leu Ala Val
 -20 -15 -10

Gly Ala Val Pro Val Val Leu Ser Ala Met Gly Phe Thr Gly Ala Gly
 -5 1 5

Ile Ala Ala Ser Ser Ile Ala Ala His Gly
 10 15

(2) INFORMATION FOR SEQ ID NO: 550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -81..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
 seq LISFSWFANYIRA/GT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550:

Met Ala Val Ile Val Asp Lys Pro Trp Phe Tyr Asp Met Lys Lys Val
 -30 -75 -70

Trp Glu Gly Tyr Pro Ile Gln Ser Thr Ile Pro Ser Gln Tyr Trp Tyr
 -65 -60 -55 -50

Tyr Met Ile Glu Leu Ser Phe Tyr Trp Ser Leu Leu Phe Ser Ile Ala
 -45 -40 -35

Ser Asp Val Lys Arg Lys Asp Phe Lys Glu Gln Ile Ile His His Val
 -30 -25 -20

Ala Thr Ile Ile Leu Ile Ser Phe Ser Trp Phe Ala Asn Tyr Ile Arg
 -15 -10 -5

Ala Gly Thr Leu Ile Met Ala Leu His Asp Ser Ser Asp Tyr Leu Leu
 1 5 10 15

Glu Ser Ala Lys Met Phe Asn Tyr Ala Gly Trp Lys Asn Thr Cys Asn
 20 25 30

Asn Ile Phe Thr Val Phe Ala Ile Val Phe Ile Ile Thr Arg Leu Val
 35 40 45

Ile Leu Pro Phe Trp Ile Leu His Cys
 50 55

(2) INFORMATION FOR SEQ ID NO: 551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq SLFIYIFLTCSNT/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551:

Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr Cys Ser Asn Thr
-15 -10 -5

Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly Leu Pro Ser Ala
1 5 10 15

Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg Leu Phe
20 25 30

Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro Leu His Leu Ile
35 40 45

Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser Gly Thr
50 55 60

(2) INFORMATION FOR SEQ ID NO: 552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq LQMLLG FVGRSKS/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552:

```
Met Ala Ala Glu Leu Val Glu Ala Lys Asn Met Val Met Ser Phe Arg  
-30 -25 -20
```

Val Ser Asp Leu Gln Met Leu Leu Gly Phe Val Gly Arg Ser Lys Ser
-15 -10 -5

Gly Leu Lys His Glu Leu Val Thr Arg Ala Leu Gln Leu Val Gln Phe
1 5 10 15

Asp Cys Ser Pro Glu Leu Phe Lys Lys Ile Lys Glu Leu Tyr Glu Thr
20 25 30

Arg Tyr Ala Lys Lys Asn Ser Glu Pro Ala Pro Gln Pro His Arg Pro
35 40 45

Leu Asp Pro Leu Thr Gly
50

(2) INFORMATION FOR SEQ ID NO: 553:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -60..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq VHALCPLSPLVTT/GC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553:

```
Met Thr Gly Leu Ser Met Xaa Gly Gly Gly Ser Xaa Xaa Gly Asp Val  
-60 -55 -50 -45
```

Xaa Pro Xaa Tyr Tyr Gly Lys Xaa Gly Pro Leu Arg Xaa Leu Pro Glu
-40 -35 -30

Pro Ser Gly Pro Leu Pro Pro Ser Ser Gly Leu Ser Gln Pro Gln Val
-25 -20 -15

His Ala Leu Cys Pro Leu Ser Pro Leu Val Thr Thr Gly Cys Cys Gly
-10 -5 1

Gln Ala Ala

(2) INFORMATION FOR SEQ ID NO: 554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq GLLGXGLXXXSLT/AG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554:

Met Gln Met Tyr Ser Arg Gln Leu Ala Ser Xaa Glu Trp Leu Thr Ile
-30 -25 -20

Gln Gly Gly Leu Leu Gly Xaa Gly Leu Xaa Xaa Xaa Ser Leu Thr Ala
-15 -10 -5 1

Gly

(2) INFORMATION FOR SEQ ID NO: 555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -54..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq LIVWLLVKSFSES/GI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555:

Met Ala Ser Leu Glu Val Ser Arg Ser Pro Arg Arg Ser Arg Arg Glu

-50 -45 -40
 Leu Glu Val Arg Ser Pro Arg Gln Asn Lys Tyr Ser Val Leu Leu Pro
 -35 -30 -25
 Thr Tyr Asn Glu Arg Glu Asn Leu Pro Leu Ile Val Trp Leu Leu Val
 -20 -15 -10
 Lys Ser Phe Ser Glu Ser Gly Ile Asn Tyr Glu Ile Ile Ile Ile Asp
 -5 1 5 10
 Asp Gly Ser Pro Asp Gly Thr Arg Asp Val Ala Glu Gln Leu Glu Lys
 15 20 25
 Ile Tyr Gly Ser Asp Arg Ile Leu Leu Arg Pro Arg Glu Lys Lys Leu
 30 35 40
 Gly Leu Gly Thr Ala Tyr Ile Xaa Xaa Met Lys His Ala Gln Glu Thr
 45 50 55
 Thr Ser Leu Leu Trp Xaa Leu Ile Ser His
 60 65

(2) INFORMATION FOR SEQ ID NO: 556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq LLDSSLMASGTAS/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556:

Met Asp Lys Asp Ser Gln Gly Leu Leu Asp Ser Ser Leu Met Ala Ser
 -20 -15 -10 -5
 Gly Thr Ala Ser Arg Ser Glu Asp Glu Glu Ser Leu Ala Gly Gln Lys
 1 5 10
 Arg Ala Ser Ser Gln Ala Leu Gly Thr Gly
 15 20

(2) INFORMATION FOR SEQ ID NO: 557:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 83 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -36..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.2
 seq CLAVSWEAAGCHG/AG
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557:

```
Met Gly Leu Leu Thr Phe Gly Tyr Ile Glu Xaa Xaa Xaa Lys Thr Glu
  -35                -30                -25

His Asn Pro Asp His His Ser Cys Leu Ala Val Ser Trp Glu Ala Ala
 -20                -15                -10                -5

Gly Cys His Gly Ala Gly Thr Gln Gln Ser Pro Leu Gly Val Ala Gly
          1                5                10

Pro Trp Arg Pro Arg Pro Pro Cys Val Gly Ser Leu Leu Ala Ala Arg
   15                20                25

Ser Leu His Lys Gln Val Ile Leu Phe Gly Leu Leu Gly Phe Ala Tyr
   30                35                40

Asp His Trp
  45
```

(2) INFORMATION FOR SEQ ID NO: 558:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Dystrophic muscle
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -16..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.1
 seq YAAVAGVLAGVES/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558:

```

Met Gly Leu Tyr Ala Ala Val Ala Gly Val Leu Ala Gly Val Glu Ser
-15                      -10                      -5

Arg Gln Gly Ser Asn Gln Gly Ala Gly Val Leu Gln Gln Leu Pro Glu
 1                      5                      10                      15

Arg Glu Xaa Ala Val Arg Ala Gly Val Arg Xaa Ala Ala Leu Leu Arg
                20                      25                      30

Arg Ala Gly Xaa Arg Asp Leu Gln Arg Arg Pro Pro Gln Cys Glu Glu
 35                      40                      45

Ala

```

(2) INFORMATION FOR SEQ ID NO: 559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -62..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq LDAVIASAGLLRA/EK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559:

```

Met Gly Leu Tyr Ala Ala Ala Ala Gly Val Leu Ala Gly Val Glu Ser
-60                      -55                      -50

Arg Gln Gly Ser Ile Lys Gly Leu Val Tyr Ser Ser Asn Phe Gln Asn
-45                      -40                      -35

Val Lys Gln Leu Tyr Ala Leu Val Cys Glu Thr Gln Arg Tyr Ser Ala
-30                      -25                      -20                      -15

Val Leu Asp Ala Val Ile Ala Ser Ala Gly Leu Leu Arg Ala Glu Lys
-10                      -5                      1

Lys Leu Arg Pro His Leu Ala Lys Val Leu Val Tyr Glu Leu Leu Leu
 5                      10                      15

Gly Lys Gly Phe Arg Gly Gly Gly Gly Arg Trp Lys Ala Arg
 20                      25                      30

```

(2) INFORMATION FOR SEQ ID NO: 560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -64..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq WLLRLAYLADIFT/KL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560:

```

Met Gly Ala Gln His Thr Ala Leu Leu Leu Asn Thr Glu Val Arg Trp
              -60                      -55                      -50

Leu Ser Arg Gly Lys Val Leu Val Arg Leu Phe Glu Leu Arg Arg Glu
              -45                      -40                      -35

Leu Leu Val Phe Met Asp Ser Ala Phe Arg Leu Ser Asp Cys Leu Thr
              -30                      -25                      -20

Asn Ser Ser Trp Leu Leu Arg Leu Ala Tyr Leu Ala Asp Ile Phe Thr
              -15                      -10                      -5

Lys Leu Asn Glu Val Asn Leu Ser Met Gln Gly Lys Asn Val Thr Val
  1              5              10              15

Phe Thr Val Phe Asp Lys Met Ser Ser Leu Leu Arg Lys Leu Glu Phe
              20              25              30

Trp Ala Ser Ser Val Glu Glu Glu Asn Phe Asp Cys Phe Pro Thr Leu
              35              40              45

Ser Asp Phe Leu Thr Glu Ile Asn Ser Thr Val Asp Lys Asp Ile Cys
              50              55              60

Ser Ala Ile Val Gln His Leu Arg Gly Leu Arg Ala Thr Leu Leu Lys
              65              70              75              80

Tyr Phe Pro Val Thr Asn Asp
              85

```

(2) INFORMATION FOR SEQ ID NO: 561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq LVVMVPLVGLIHL/GW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561:

Met Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu Val Val Met
-25 -20 -15 -10

Val Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg Ile Lys Ser
 -5 1 5

Ser Pro Val Phe Gln Ile Pro Lys Asn Asp Asn Met
 10 15

(2) INFORMATION FOR SEQ ID NO: 562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -51..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq GKLLQLVLGCAIS/CE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562:

Met Val Leu Arg Ser Leu Val Glu Tyr Ser Gln Asp Val Leu Ala His
-50 -45 -40

Pro Val Ser Glu Glu His Leu Pro Asp Val Ser Leu Ile Gly Glu Phe
-35 -30 -25 -20

Ser Asp Pro Ala Glu Leu Gly Lys Leu Leu Gln Leu Val Leu Gly Cys

-15 -10 -5
Ala Ile Ser Cys Glu Lys Lys Gln Asp His Ile Gln Arg Ile Met Thr
 1 5 10
Leu Glu Glu Ser Val Gln His Val Val Met Glu Ala Ile Gln Glu Leu
 15 20 25
Met Thr Lys Asp Thr Pro Asp Ser Leu Ser Pro Glu Thr Tyr Gly Asn
 30 35 40 45
Phe Asp Ser Gln Ser Arg Ser Thr Gly
 50

(2) INFORMATION FOR SEQ ID NO: 563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -13..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq MIHGFCLAPTTSA/KN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563:

Met Ile His Gly Phe Cys Leu Ala Pro Thr Thr Ser Ala Lys Asn Ala
 -10 -5 1

(2) INFORMATION FOR SEQ ID NO: 564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: -17..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: . score 3.7
 seq RTWCLACVEASPG/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:

Met Xaa Cys Pro Arg Thr Trp Cys Leu Ala Cys Val Glu Ala Ser Pro
 -15 -10 -5

Gly Gln Pro Phe Leu Pro Pro Arg Pro Gly
 1 5

(2) INFORMATION FOR SEQ ID NO: 565:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -21..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.7
 seq ETCALASHSGSSG/SK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 -20 -15 -10

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
 -5 1 5 10

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
 15 20 25

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Xaa Arg Cys
 30 35 40

Gln Ala Gly
 45

(2) INFORMATION FOR SEQ ID NO: 566:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids
 (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN .

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -26..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq IIMFLLIIVCGSP/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566:

Met Phe Lys Val Ala Ala Pro Pro Met Leu Ile Xaa Xaa Ile Ile Met
-25 -20 -15

Phe Leu Leu Ile Ile Val Cys Gly Ser Pro Arg Pro
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 567:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq FXMCLWSLRNLFS/RC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567:

Met Asp Phe Trp Asp Pro Ala Val Phe Xaa Met Cys Leu Trp Ser Leu
-20 -15 -10

Arg Asn Leu Phe Ser Arg Cys Ser Pro Cys Leu Thr Glu Ile Ser Leu
-5 1 5 10

His Leu Val His Leu Thr Ala Glu Lys Lys Gln His Gly Ser Asn Asn
15 20 25

Gly Ser Ala
30

(2) INFORMATION FOR SEQ ID NO: 568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -34..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq SVPLLSLSHSIGI/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568:

Met Ser Pro Ala Gly Lys His Asn Ser Glu Ser Lys Phe Thr Phe Phe
 -30 -25 -20

Val Ala Leu Asp Gly Ser Val Pro Leu Leu Ser Leu Ser His Ser Ile
 -15 -10 -5

Gly Ile Ser Pro Thr Arg
 1

(2) INFORMATION FOR SEQ ID NO: 569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq LVCVGLHTEGPWG/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:

Met His Trp Ala Leu Val Cys Val Gly Leu His Thr Glu Gly Pro Trp
 -15 -10 -5

Gly Arg Pro Ser Gly Leu Ala Ser Ala Ser Gly Met Asp Arg Ala Arg
 1 5 10 15

Gln Ala Ser Glu Leu Pro Pro Pro Gly Ala Ser Gln Thr Pro Gln
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -72..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq WFYIGSSLNGTRG/KR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:

Met Phe Gly Ala Ala Ala Arg Ser Ala Asp Leu Val Leu Leu Glu Lys
 -70 -65 -60

Asn Leu Gln Ala Ala His Gly Tyr Ala Gln Glu Asp Arg Glu Arg Met
 -55 -50 -45

His Arg Xaa Ile Val Ser Leu Xaa Gln Asn Leu Leu Asn Phe Met Ile
 -40 -35 -30 -25

Gly Ser Ile Leu Asp Leu Trp Gln Cys Phe Leu Trp Phe Tyr Ile Gly
 -20 -15 -10

Ser Ser Leu Asn Gly Thr Arg Gly Lys Arg Val Pro Ala His Phe
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Heart .

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -27..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq VVALLIVCDVPSA/SA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:

```

Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val Val
  -25                -20                -15

Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Arg
  -10                -5                1

```

(2) INFORMATION FOR SEQ ID NO: 572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq LLLQPSMIQEVWT/XY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

```

Met Val Val Leu Leu Leu Gln Pro Ser Met Ile Gln Glu Val Trp Thr
  -15                -10                -5

Xaa Tyr Ala Asn Leu Phe His Ser Phe Phe Val Asp Asn Pro Phe Gln
  1                5                10                15

Lys Glu Cys Phe His Gln Lys Asn Trp Tyr His Ile Thr Leu Met Gln
  20                25                30

Arg Thr Val Gly Thr Trp Arg Ile Leu Pro Asn Phe Leu Lys His Asp
  35                40                45

```

(2) INFORMATION FOR SEQ ID NO: 573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.5
seq LAVLLSLAPSASS/DI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573:

Met Leu His Leu His Xaa Ser Cys Leu Cys Phe Arg Ser Trp Leu Pro
-30 -25 -20

Ala Met Leu Ala Val Leu Leu Ser Leu Ala Pro Ser Ala Ser Ser Asp
-15 -10 -5 1

Ile Ser Ala Ser Arg Pro Asn Ile Leu Leu Leu Met Ala Asp Asp Leu
5 10 15

Gly Ile Gly Asp Ile Gly Cys Tyr Gly Asn Asn Thr Met Arg Thr Pro
20 25 30

Xaa Ile Asp Arg Leu Ala Glu Asp Gly Val Lys Leu Thr Gln His Ile
35 40 45

Ser Ala Ala Ser Leu Cys
50 55



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/12, C07K 14/47	A3	(11) International Publication Number: WO 99/06554 (43) International Publication Date: 11 February 1999 (11.02.99)
(21) International Application Number: PCT/IB98/01238 (22) International Filing Date: 31 July 1998 (31.07.98) (30) Priority Data: 08/905,134 1 August 1997 (01.08.97) US (71) Applicant (for all designated States except US): GENSET [FR/FR]; 24, rue Royale, F-75008 Paris (FR). (72) Inventors; and (75) Inventors/Applicants (for US only): DUMAS MILNE ED- WARDS, Jean-Baptiste [FR/FR]; 8, rue Grégoire de Tours, F-75006 Paris (FR). DUCLERT, Aymeric [FR/FR]; 6 ter, rue Victorine, F-94100 Saint-Maur (FR). LACROIX, Bruno [FR/FR]; 93, route de Vourles, F-69230 Saint-Genis Laval (FR). (74) Agents: MARTIN, Jean-Jacques et al.; Cabinet Regimbeau, 26, avenue Kléber, F-75116 Paris (FR).		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> (88) Date of publication of the international search report: 27 May 1999 (27.05.99)
(54) Title: 5' ESTs FOR SECRETED PROTEINS EXPRESSED IN MUSCLE AND OTHER MESODERMAL TISSUES (57) Abstract The sequences of 5' ESTs derived from mRNAs encoding secreted proteins are disclosed. The 5' ESTs may be to obtain cDNAs and genomic DNAs corresponding to the 5' ESTs. The 5' ESTs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. Upstream regulatory sequences may also be obtained using the 5' ESTs. The 5' ESTs may also be used to design expression vectors and secretion vectors.		

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DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 98/01238

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12N15/12 C07K14/47

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
E	WO 98 44114 A (INCYTE PHARMACEUTICALS INC. (US); HILLMAN JENNIFER L.; GOLI SURYA K.) 8 October 1998 see abstract see page 12, line 5-14 see page 42 - page 43 see page 46 - page 47; claims --- -/-	1-11, 15-37

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents:

A document defining the general state of the art which is not considered to be of particular relevance

E earlier document but published on or after the international filing date

L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

O document referring to an oral disclosure, use, exhibition or other means

P document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

Z document member of the same patent family

Date of the actual completion of the international search

10 November 1998

Date of mailing of the international search report

01 03 99

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

Authorized officer

Macchia, G

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
E	<p>WO 98 42738 A (HUMAN GENOME SCIENCES INC. (US); YOUNG PAUL ET AL.) 1 October 1998 see page 40, line 34 - page 41, line 35 Gene No.46 see page 79 see page 100, line 23-25 Seq.ID:56 see page 209 - page 210 Seq.ID:110 see page 259 - page 260 Seq.ID:170 see page 297 - page 298 Seq.ID:224 see page 331 - page 332 see page 381 - page 384; claims ---</p>	<p>1-28, 34-37</p>
X	<p>Database EMBL Emest7, Entry HS1150166 Accession number AA232452 6 March 1997 96% identity with Seq.ID:38 nt.41-140 XP002083765</p>	<p>1-11, 15-37</p>
Y	<p>see the whole document ---</p>	<p>12-14</p>
Y	<p>YOKOYAMA-KOBAYASHI M. ET AL.: "A signal sequence detection system using secreted protease activity as an indicator" GENE, vol. 163, 1995, pages 193-196, XP002053953 see abstract ---</p>	<p>12,13</p>
Y	<p>LIN Y. ET AL.: "Inhibition of nuclear translocation of transcription factor NF-kB by a synthetic peptide containing a cell membrane-permeable motif and nuclear localization sequence" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 270, no. 24, 16 June 1995, pages 14255-14258, XP002050723 cited in the application see abstract ---</p>	<p>14</p>
A	<p>OZAWA M.: "Cloning of a human homologue of mouse reticulocalbin reveals conservation of structural domains in the novel endoplasmic reticulum resident Ca²⁺-binding protein with multiple EF-hand motifs" JOURNAL OF BIOCHEMISTRY, vol. 117, 1995, pages 1113-1119, XP002070128 ---</p>	

-/--

INTERNATIONAL SEARCH REPORT

Application No

PCT/IB 98/01238

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	SCHÄFER B.W. AND HEIZMANN C.W.: "The S100 family of EF-hand calcium-binding proteins: functions and pathology" TIBS TRENDS IN BIOCHEMICAL SCIENCES, vol. 21, no. 4, April 1996, page 134-140 XP004050923 ---	
A	WO 96 34981 A (GENSET (FR); MERENKOVA IRENA NICOLAEVNA; DUMAS MILNE EDWARDS JEAN) 7 November 1996 cited in the application ---	
A	KATO S. ET AL.: "Construction of a human full-length cDNA bank" GENE, vol. 150, 1994, pages 243-250, XP002081364 cited in the application ---	
A	EP 0 625 572 A (KANAGAWA ACAD OF SCIENCE AND TECHNOL FOUNDATION (JP); KATO S; SEKINE S) 23 November 1994 cited in the application ---	
A	CARNINCI P. ET AL.: "High-efficiency full-length cDNA cloning by biotinylated CAP trapper" GENOMICS, vol. 37, no. 3, 1 November 1996, pages 327-336, XP002081729 cited in the application ---	
A	WO 97 07198 A (GENETICS INSTITUTE INC (US); JACOBS K; MCCOY JM; KELLEHER K; CARLIN M) 27 February 1997 ---	
A	TASHIRO K. ET AL.: "Signal sequence trap: a cloning strategy for secreted proteins and type I membrane proteins" SCIENCE, vol. 261, 30 July 1993, pages 600-603, XP000673204 ---	
A	HEIJNE VON G.: "A new method for predicting signal sequence cleavage sites" NUCLEIC ACIDS RESEARCH, vol. 14, no. 11, 1986, pages 4683-4690, XP002053954 cited in the application -----	

INTERNATIONAL SEARCH REPORT

International application No.

PCT/IB 98/01238

B x I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

B x II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

See extra sheet, Invention 1.

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: Claims 1-37 all partially

Nucleic acid comprising the sequence as in Seq.ID:38, complementary sequence, fragments, hybridizing sequences. Polypeptide comprising a signal peptide encoded by said nucleotide sequence. Vector encoding a fusion protein comprising said signal peptide. A method of directing the extracellular secretion of a polypeptide by means of said vector. Method of importing a polypeptide into a cell by means of said signal peptide. A method for making a cDNA encoding a secretory protein, partially encoded by said nucleotide sequence, corresponding cDNA. Polypeptide encoded by said nucleotide sequence, comprising a sequence as in Seq.ID:306, method of making said polypeptide. Method of obtaining a promoter located upstream of said nucleotide sequence, promoter thereof.

Inventions 2-268: Claims 1-37 all partially

Idem as subject 1 but limited to each of the DNA sequences as in Seq.ID:39-305, and corresponding polypeptides, where invention 2 is limited to Seq.ID:39 and 307, invention 3 is limited to Seq.ID:40 and 308,....., invention 147 is limited to Seq.ID:305 and 573).

For the sake of conciseness, the first subject matter is explicitly defined, the other subject matters are defined by analogy thereto.

INTERNATIONAL SEARCH REPORT

Information on patent family members

Application No

PCT/IB 98/01238

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9844114 A	08-10-1998	AU 6787598 A	22-10-1998
WO 9842738 A	01-10-1998	AU 6564698 A	12-10-1998
		AU 6562798 A	20-10-1998
WO 9634981 A	07-11-1996	FR 2733765 A	08-11-1996
		FR 2733762 A	08-11-1996
		AU 5982996 A	21-11-1996
		CA 2220045 A	07-11-1996
		EP 0824598 A	25-02-1996
EP 0625572 A	23-11-1994	JP 6153953 A	03-06-1994
		WO 9408001 A	14-04-1994
		US 5597713 A	28-01-1997
WO 9707198 A	27-02-1997	US 5707829 A	13-01-1998
		AU 6712396 A	18-02-1997
		AU 6768596 A	12-03-1997
		CA 2227220 A	06-02-1997
		CA 2229208 A	27-02-1997
		EP 0839196 A	06-05-1998
		EP 0851875 A	08-07-1998
		WO 9704097 A	06-02-1997

ID AI022447 standard; RNA; EST; 343 BP.

XX

AC AI022447;

XX

SV AI022447.1

XX

DT 19-JUN-1998 (Rel. 56, Created)

DT 03-MAR-2000 (Rel. 63, Last updated, Version 3)

XX

DE ow96g09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
DE clone IMAGE:1654720 3', mRNA sequence.

XX

KW EST.

XX

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Teleostomi;

OC Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX

RN [1]

RP 1-343

RA NCI-CGAP;

RT "National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor

RT Gene Index <http://www.ncbi.nlm.nih.gov/ncicgap>;

RL Unpublished.

XX

DR RZPD; IMAGp998H174199; IMAGp998H174199.

XX

CC On Jan 19, 1998 this sequence version replaced gi:2153386.

CC Contact: Robert Strausberg, Ph.D.

CC Tel: (301) 496-1550

CC Email: Robert_Strausberg@nih.gov

CC This clone is available royalty-free through LLNL ; contact the

CC IMAGE Consortium (info@image.llnl.gov) for further information.

CC Insert Length: 966 Std Error: 0.00

CC Seq primer: -40m13 fwd. ET from Amersham

CC High quality sequence stop: 342.

XX

FH Key Location/Qualifiers

FH

FT source

FT

FT /db_xref="taxon:9606"

FT

FT /db_xref="ESTLIB:452"

FT

FT /db_xref="RZPD:IMAGp998H174199"

FT

FT /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)

FT

FT with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;

FT

FT This is a subtracted version of the original Soares fetal

FT

FT liver spleen 1NFLS library. 1st strand cDNA was primed

FT

FT with a Pac I - oligo(dT) primer [5'

FT

FT AACTGGAAGAATTAATTAAGATCTTTTTTTTTTTTTTTTTTTT 3'],

FT

FT double-stranded cDNA was ligated to Eco RI adaptors

FT

FT (Pharmacia), digested with Pac I and cloned into the Pac I

FT

FT and Eco RI sites of the modified pT7T3 vector. Library

FT

FT went through one round of normalization. Library

FT

FT constructed by Bento Soares and M.Fatima Bonaldo."

FT

FT /sex="male"

FT

FT /organism="Homo sapiens"

FT

FT /clone="IMAGE:1654720"

FT

FT /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"

FT

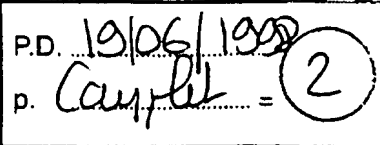
FT /dev_stage="20 week-post conception fetus"

FT

FT /lab_host="DH10B (ampicillin resistant)"

XX

SQ Sequence 343 BP; 61 A; 102 C; 94 G; 86 T; 0 other;



Ai022447 Length: 343 April 28, 19100 17:03 Type: N Check: 7920 ..

1 TAGAGACAGT GCGGTTTATC ACCCTCAACC AGGCCTGGCT TGGGCTTCAC
51 TGTAACGTG TGACGTGGGG CCAGTGGATC ACTTGGGTGC CTCAATTGG
101 CCTCTTCTAC CCATGTGCAG GCTGGTAGGG CAGTCGGGT TGGCATCTGG
151 TGAGGTTCCC CCTATTGTAC CCAGTTACGG CCCCCTCCC CACCATTTC
201 CAGCCTCCTG TTGCCCCTCT CCCTGTGGAG ACGCTGCCTG TGGAAAGGG
251 CCTCCTTCTG GTCATGGCT CCCTTCTTGC AGCTGGAGGA ATGGGAGCTC
301 AAAAAGAACT TCCTAGTAGC AGCCAGTCAG CATCTTCGAA AAG

XP-002136769

PD	1996	1
p.		

(C) BIOSIS / BIOSIS

AN - PREV199699135023
TI - Cloning of cDNA encoding human rapsyn and mapping of the
RAPSN gene locus to chromosome 11p11.2-p11.1.
AU - Buckel Alex; Beeson David; James Michael; Vincent Angela
AUAF- Neurosciences Group, Inst. Molecular Med., John Radcliffe Hosp.,
Headington, Oxford OX3 9DU;
- UK
PUB - Genomics
- 1996
VOL - 35
PG - 613-616
AB - We have isolated and sequenced cDNA clones for the human 43-kDa
acetylcholine receptor-associated protein rapsyn. The cDNA
encodes a 412-amino-acid protein that has a predicted molecular mass
of 46,330 Da and shows 96% sequence identity with mouse rapsyn.
Analysis of PCR amplifications, first from somatic cell hybrids and
subsequently from radiation hybrids, localizes the human RAPSN
gene locus to chromosome 11p11.2-p11.1 in close proximity to ACP2.

